

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 14, 2003, 13:44:04 ; Search time 34 Seconds
(without alignments)
1412.029 Million cell updates/sec

Title: US-09-869-136-2
Perfect score: 1207
Sequence: 1 MKTKLIFSFTSIFALISR.....KDNKSFNIDKIGHLDIEIDS 233

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues 671580

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_21.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|--------|--------------------|
| 1 | 1157 | 95.9 | 256 | Q9SLH8 | Q9slh8 streptococc |
| 2 | 1126 | 93.3 | 233 | Q99XW1 | Q99xw1 streptococc |
| 3 | 1091 | 90.4 | 209 | Q9RQK5 | Q9rqk5 streptococc |
| 4 | 1070 | 88.6 | 209 | Q9LAD8 | Q9lad8 streptococc |
| 5 | 1069 | 88.6 | 209 | Q9LAE0 | Q9lae0 streptococc |
| 6 | 1069 | 88.6 | 209 | Q9LAC6 | Q9lac6 streptococc |
| 7 | 1069 | 88.6 | 209 | Q9LAC5 | Q9lac5 streptococc |
| 8 | 1066 | 88.3 | 209 | Q9LAE1 | Q9lae1 streptococc |
| 9 | 1063 | 88.1 | 256 | Q9XR88 | Q9xr88 streptococc |
| 10 | 1062 | 88.0 | 209 | Q9LAC4 | Q9lac4 streptococc |
| 11 | 1060 | 87.8 | 209 | Q9LAD6 | Q9lad6 streptococc |
| 12 | 1059 | 87.7 | 209 | Q9LAD2 | Q9lad2 streptococc |
| 13 | 1059 | 87.7 | 256 | Q9SLH9 | Q9slh9 streptococc |
| 14 | 1058 | 87.7 | 209 | Q9LAD1 | Q9lad1 streptococc |
| 15 | 1055 | 87.4 | 209 | Q9LAC7 | Q9lac7 streptococc |
| 16 | 1054 | 87.3 | 209 | Q9LAC9 | Q9lac9 streptococc |

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17 1052 87.2 209 2 Q9LAC3 streptococc
18 1046 86.7 209 2 Q9LAC8 streptococc
19 1042 86.3 209 2 Q9LAD4 streptococc
20 1038 85.2 209 2 Q9LAD7 streptococc
21 1027 85.1 209 2 Q9LAD5 streptococc
22 1027 85.1 209 2 Q9LAD3 streptococc
23 1018 84.3 209 2 Q9LAD9 streptococc
24 1015 84.1 209 2 Q9LAD0 streptococc
25 310.5 25.7 256 2 Q9VLW7 streptococc
26 309.5 25.6 242 2 Q93CC6 streptococc
27 308 25.5 240 16 Q9F0L7 streptococc
28 300.5 24.9 242 2 Q94476 streptococc
29 297.5 24.6 242 16 Q95383 streptococc
30 295.5 24.5 242 2 Q93CC5 streptococc
31 283.5 23.5 218 2 Q9RR75 streptococc
32 276 22.9 239 2 Q9EZM7 streptococc
33 274 22.7 239 16 Q99T47 streptococc
34 262 21.7 206 2 Q94512 streptococc
35 259 21.5 232 16 Q99QN1 streptococc
36 251.5 20.8 260 16 Q931M4 streptococc
37 240 19.9 210 2 Q9K2G9 streptococc
38 238.5 19.8 225 2 Q9VVM1 streptococc
39 238.5 19.8 225 16 Q99Z21 streptococc
40 236.5 19.6 225 2 Q9L921 streptococc
41 232 19.2 234 2 Q93RR9 streptococc
42 231.5 19.2 268 2 Q95217 streptococc
43 231 19.1 260 16 Q99SU3 streptococc
44 217.5 18.0 241 2 Q93585 streptococc
45 210.5 17.4 236 2 Q94696 streptococc

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ALIGNMENTS

RESULT 1

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Q9SLH8 ID Q9SLH8 PRELIMINARY; PRT; 256 AA.
AC Q9SLH8;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE SPEX protein precursor.
GN SPEX.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=12714 TYPE 12;
RX MEDLINE=20374978; PubMed=10913699;
RA Gerlach D., Fleischer B., Wagner M., Schmidt K.H., Vettermann S.,
RA Reichardt W.;
RT "Purification and Biochemical Characterization of a Basic Superantigen
(RL FEMS Microbiol. Lett. 188:153-163(2000).
RL EMBL; AJ245405; CAB51744.1;
DR NSSP; P13163; 1SXT.
DR InterPro; IPR001361; Strep/Strep_Coxin.
DR Pfam; PF01123; Strep_Strep_Toxin; 1.
DR Pfam; PF02876; Strep_Strep_Tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW SIGNAL.
FT SIGNAL.
SQ SEQUENCE 256 AA; 29706 MW; 873D0BAFBE6DC332 CRC64;
Query Match 95.9%; Score 1157; DB 2; Length 256;
Best Local Similarity 97.0%; Pred. No. 1.6e-77;
Matches 226; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 MKTKLIFSFTSIFALISRPFVGLVDNNSLLRNYSIVVEYSDIVDFKTSNHLVTK 60
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Db 24 MKTKLIFSFTSIFAIISRPVGLVNDNLSLNRYSTIVYEYSDIVDFKSHNLVTK 83
QY 61 KLDVRDARDFFINSEMDYAAANDFKTGDKIAVESVPDWNLYLSKGVYATYTGITPYQK 120
Db 84 KLDVRDARDFFINSEMDYAAANDFKTGDKIAVESVPDWNLYLSKGVYATYTGITPYQK 143
QY 121 TSPKNTPVNLWNGKQISVPYNEISTNKTVTAAQIEDLKVRFELIAHQHLYSGSSYKS 180
Db 144 LOYKLSLWNLWNGKQISVPYNEISTNKTVTAAQIEDLKVRFELIAHQHLYSGSSYKS 203
QY 181 GRLVFHTNDSKYSFDFLVGVYRDKEISFKVYKDNKSFNIDKIGHLDIEIDS 233
Db 204 GRLVFHTNDSKYSFDFLVGVYRDKEISFKVYKDNKSFNIDKIGHLDIEIDS 256

RESULT 2
Q99XW1
ID Q99XW1 PRELIMINARY; PRT; 233 AA.
AC Q99XW1;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Mitogenic exotoxin 2.
GN SMEZ OR spyi998.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2035;
RX MEDLINE=99093428; PubMed=9874566;
RA Profit T., Moffatt S.L., Berkahn C.J., Fraser J.D.;
RT "Identification and characterization of novel superantigens from
RL Streptococcus pyogenes.";
RL J. Exp. Med. 189:89-102(1999).
DR EMBL: AF086626; AAD52087.1;
DR HSSP: P13163; LSXT.
DR InterPro: IPR001961; Strep/Strep-toxin.
DR Pfam: PF01123; Strep_Strp_toxin; 1.
DR Pfam: PF02876; Strep_Strp_tox_C; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 209 AA; 24131 MW; 52BF7911BB100152 CRC64;

Query Match 90.4%; Score 1091; DB 2; Length 209;
Best Local Similarity 100.0%; Pred. No. 8.e-73;
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 LEVDNNSLLRNISTIVYEYSDIVDFKSHNLVTKKLDVRDARDFFINSEMDYAAANDF 84
Db 1 LEVDNNSLLRNISTIVYEYSDIVDFKSHNLVTKKLDVRDARDFFINSEMDYAAANDF 60
QY 85 KTGDKIAVESVPDWNLYLSKGVYATYTGITPYQKTSIPKNIPVNLWNGKQISVPYNE 144
Db 61 KTGDKIAVESVPDWNLYLSKGVYATYTGITPYQKTSIPKNIPVNLWNGKQISVPYNE 120
QY 145 ISTNKTVTAAQIEDLKVRFELIAHQHLYSGSSYKSGLVYFHTNDSKYSFDFLVYGYR 204
Db 121 ISTNKTVTAAQIEDLKVRFELIAHQHLYSGSSYKSGLVYFHTNDSKYSFDFLVYGYR 180
QY 205 DKESIFKVKDNKSFNIDKIGHLDIEIDS 233
Db 181 DKESIFKVKDNKSFNIDKIGHLDIEIDS 209

RESULT 4
Q9LAD8
ID Q9LAD8 PRELIMINARY; PRT; 209 AA.
AC Q9LAD8;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Mitogenic exotoxin 2-7 (Fragment).
GN SMEZ-7.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=11574;
RX MEDLINE=20733982; PubMed=10811869;
RA Profit T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
RL Mosaic Structure, and Significant Antigenic Variation.";
RL J. Exp. Med. 191:1765-1776(2000).
DR EMBL: AF143657; AAF66657.1;
DR HSSP: P13163; LSXT.
DR InterPro: IPR001961; Strep/Strep-toxin.

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Db 24 MKTKLIFSFTSIFAIISRPVGLVNDNLSLNRYSTIVYEYSDIVDFKSHNLVTK 83
QY 61 KLDVRDARDFFINSEMDYAAANDFKTGDKIAVESVPDWNLYLSKGVYATYTGITPYQK 120
Db 84 KLDVRDARDFFINSEMDYAAANDFKTGDKIAVESVPDWNLYLSKGVYATYTGITPYQK 143
QY 121 TSPKNTPVNLWNGKQISVPYNEISTNKTVTAAQIEDLKVRFELIAHQHLYSGSSYKS 180
Db 144 LOYKLSLWNLWNGKQISVPYNEISTNKTVTAAQIEDLKVRFELIAHQHLYSGSSYKS 203
QY 181 GRLVFHTNDSKYSFDFLVGVYRDKEISFKVYKDNKSFNIDKIGHLDIEIDS 233
Db 204 GRLVFHTNDSKYSFDFLVGVYRDKEISFKVYKDNKSFNIDKIGHLDIEIDS 256

RESULT 2
Q99XW1
ID Q99XW1 PRELIMINARY; PRT; 233 AA.
AC Q99XW1;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Mitogenic exotoxin 2.
GN SMEZ OR spyi998.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2035;
RX MEDLINE=99093428; PubMed=9874566;
RA Profit T., Moffatt S.L., Berkahn C.J., Fraser J.D.;
RT "Identification and characterization of novel superantigens from
RL Streptococcus pyogenes.";
RL J. Exp. Med. 189:89-102(1999).
DR EMBL: AF086626; AAD52087.1;
DR HSSP: P13163; LSXT.
DR InterPro: IPR001961; Strep/Strep-toxin.
DR Pfam: PF01123; Strep_Strp_toxin; 1.
DR Pfam: PF02876; Strep_Strp_tox_C; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 209 AA; 24131 MW; 52BF7911BB100152 CRC64;

Query Match 93.3%; Score 1126; DB 16; Length 233;
Best Local Similarity 92.7%; Pred. No. 2.7e-75;
Matches 216; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 1 MKTKLIFSFTSIFAIISRPVGLVNDNLSLNRYSTIVYEYSDIVDFKSHNLVTK 60
Db 1 MKTKLIFSFTSIFAIISRPVGLVNDNLSLNRYSTIVYEYSDIVDFKSHNLVTK 60
QY 61 KLDVRDARDFFINSEMDYAAANDFKTGDKIAVESVPDWNLYLSKGVYATYTGITPYQK 120
Db 61 KLDVRDARDFFINSEMDYAAANDFKTGDKIAVESVPDWNLYLSKGVYATYTGITPYQK 120
QY 121 TSPKNTPVNLWNGKQISVPYNEISTNKTVTAAQIEDLKVRFELIAHQHLYSGSSYKS 180
Db 121 EPMKSNIPVNLWNGKQISVPYNEISTNKTVTAAQIEDLKVRFELIAHQHLYSGSSYKS 180
QY 181 GRLVFHTNDSKYSFDFLVGVYRDKEISFKVYKDNKSFNIDKIGHLDIEIDS 233
Db 181 GRLVFHTNDSKYSFDFLVGVYRDKEISFKVYKDNKSFNIDKIGHLDIEIDS 233

RESULT 3
Q9RQ05
ID Q9RQ05 PRELIMINARY; PRT; 209 AA.
AC Q9RQ05;

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DR Pfam: PF01123; Stap_Strp_toxin; 1.
DR Pfam: PF02876; Stap_Strp_tox_C; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 209 AA; 24064 MW; 67E977CD5AA934F7 CRC64;

Query Match 88.6%; Score 1070; DB 2; Length 209;
Best Local Similarity 97.6%; Pred. No. 3.7e-71;
Matches 204; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 25 LEVDNNSLLRNIIYTIYVEYSDIVDFKTSNHLVTKKLDVRDARDFINSEMDEYAANDF 84
Db 1 LEVDNNSLLRNIIYTIYVEYSDIVDFKTSNHLVTKKLDVRDARDFINSEMDEYAANDF 60

QY 85 KTGDKIAVSPFDNVLKSGKVTATYGGITPYQKTSIPKNIPVNLWINKQISVPYNE 144
Db 1 KTGDKIAVSPFDNVLKSGKVTATYGGITPYQKTSIPKNIPVNLWINKQISVPYNE 120

QY 145 ISTNKTVTVAQEIIDLKVRKFLIAQHLYSGSSYKSGRLVFHTNDNSDKYSFDFLYVGYR 204
Db 1 ISTNKTVTVAQEIIDLKVRKFLIAQHLYSGSSYKSGRLVFHTNDNSDKYSFDFLYVGYR 180

QY 205 DKESIFKVKDKNSFNIDKIGHLDIEIDS 233
Db 181 DKESIFKVKDKNSFNIDKIGHLDIEIDS 209

RESULT 5
Q9LAE0
ID Q9LAE0 PRELIMINARY; PRT; 209 AA.
AC Q9LAE0;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Mitogenic exotoxin 2-4 (Fragment).
GN SMEZ-4.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=5983;
RX MEDLINE=20273982; PubMed=10811869;
RA Prof T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
RA Fraser J.D.;
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
RT Mosaic Structure, and Significant Antigenic Variation.";
RL J. Exp. Med. 191:1765-1776(2000).
DR EMBL: AF143654; AAF66655.1; -
DR HSSP: P13163; LSXT.
DR InterPro: IPR001961; Stap/Strp-toxin.
DR Pfam: PF01123; Stap_Strp_toxin; 1.
DR Pfam: PF02876; Stap_Strp_tox_C; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 209 AA; 24108 MW; 67EC279BBCA8247 CRC64;

Query Match 88.6%; Score 1069; DB 2; Length 209;
Best Local Similarity 97.6%; Pred. No. 3.7e-71;
Matches 204; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 25 LEVDNNSLLRNIIYTIYVEYSDIVDFKTSNHLVTKKLDVRDARDFINSEMDEYAANDF 84
Db 1 LEVDNNSLLRNIIYTIYVEYSDIVDFKTSNHLVTKKLDVRDARDFINSEMDEYAANDF 60

QY 85 KTGDKIAVSPFDNVLKSGKVTATYGGITPYQKTSIPKNIPVNLWINKQISVPYNE 144
Db 1 KTGDKIAVSPFDNVLKSGKVTATYGGITPYQKTSIPKNIPVNLWINKQISVPYNE 120

QY 145 ISTNKTVTVAQEIIDLKVRKFLIAQHLYSGSSYKSGRLVFHTNDNSDKYSFDFLYVGYR 204
Db 1 ISTNKTVTVAQEIIDLKVRKFLIAQHLYSGSSYKSGRLVFHTNDNSDKYSFDFLYVGYR 180

QY 205 DKESIFKVKDKNSFNIDKIGHLDIEIDS 233
Db 181 DKESIFKVKDKNSFNIDKIGHLDIEIDS 209

RESULT 7
Q9LAC5
ID Q9LAC5 PRELIMINARY; PRT; 209 AA.
AC Q9LAC5;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Mitogenic exotoxin 2-21 (Fragment).
GN SMEZ-21.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.

Db 121 ISTNKTVTVAQEIIDLKVRKFLIAQHLYSGSSYKSGRLVFHTNDNSDKYSFDFLYVGYR 180
QY 205 DKESIFKVKDKNSFNIDKIGHLDIEIDS 233
Db 181 DKESIFKVKDKNSFNIDKIGHLDIEIDS 209

RESULT 6
Q9LAC6
ID Q9LAC6 PRELIMINARY; PRT; 209 AA.
AC Q9LAC6;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Mitogenic exotoxin 2-20 (Fragment).
GN SMEZ-20.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=10989;
RX MEDLINE=20273982; PubMed=10811869;
RA Prof T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
RA Fraser J.D.;
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
RT Mosaic Structure, and Significant Antigenic Variation.";
RL J. Exp. Med. 191:1765-1776(2000).
DR EMBL: AF143670; AAF66669.1; -
DR HSSP: P13163; LSXT.
DR InterPro: IPR001961; Stap/Strp-toxin.
DR Pfam: PF01123; Stap_Strp_toxin; 1.
DR Pfam: PF02876; Stap_Strp_tox_C; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 209 AA; 24100 MW; 53049A11599BEA68 CRC64;

Query Match 88.6%; Score 1069; DB 2; Length 209;
Best Local Similarity 97.6%; Pred. No. 3.7e-71;
Matches 204; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 25 LEVDNNSLLRNIIYTIYVEYSDIVDFKTSNHLVTKKLDVRDARDFINSEMDEYAANDF 84
Db 1 LEVDNNSLLRNIIYTIYVEYSDIVDFKTSNHLVTKKLDVRDARDFINSEMDEYAANDF 60

QY 85 KTGDKIAVSPFDNVLKSGKVTATYGGITPYQKTSIPKNIPVNLWINKQISVPYNE 144
Db 1 KTGDKIAVSPFDNVLKSGKVTATYGGITPYQKTSIPKNIPVNLWINKQISVPYNE 120

QY 145 ISTNKTVTVAQEIIDLKVRKFLIAQHLYSGSSYKSGRLVFHTNDNSDKYSFDFLYVGYR 204
Db 121 ISTNKTVTVAQEIIDLKVRKFLIAQHLYSGSSYKSGRLVFHTNDNSDKYSFDFLYVGYR 180

QY 205 DKESIFKVKDKNSFNIDKIGHLDIEIDS 233
Db 181 DKESIFKVKDKNSFNIDKIGHLDIEIDS 209

RESULT 7
Q9LAC5
ID Q9LAC5 PRELIMINARY; PRT; 209 AA.
AC Q9LAC5;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Mitogenic exotoxin 2-21 (Fragment).
GN SMEZ-21.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.

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OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RO STRAIN=11222.
RX MEDLINE=20273982; PubMed=10811869;
RA Proft T., Mofatt S.L., Weller K.D., Paterson A., Martin D.,
RA Fraser J.D.;
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
RT Mosaic Structure, and Significant Antigenic Variation.";
RL J. Exp. Med. 191:1765-1776(2000).
DR EMBL; AF143671; AAF66670.1; -.
DR HSSP; P13163; ISXT.
DR InterPro; IPR001961; Strep_Strep_toxin.
DR Pfam; PF01123; Strep_Strep_toxin; 1.
DR Pfam; PF02876; Strep_Strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER
SQ SEQUENCE 209 AA; 24106 MW; 67FD2696FA4BC55A CRC64;

Query Match 88.6%; Score 1069; DB 2; Length 209;
Best Local Similarity 97.6%; Pred. No. 3.7e-71;
Matches 204; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 25 LEVDNNSLLRNIIYTIYVEYSDIVDFKTSNHLVTKKLDVDRDARDFINSEMEYAAANDF 84
Db 1 LEVDNNSLLRNIIYTIYVEYSDIVDFKTSNHLVTKKLDVDRDARDFINSEMEYAAANDF 60
QY 85 KTGDKIAVSPFDWNLVSKGKVTAYTYGGITPYQKTSIPKNIPVNLWNGKQISVPYNE 144
Db 61 KTGDKIAVSPFDWNLVSKGKVTAYTYGGITPYQKTSIPKNIPVNLWNGKQISVPYNE 120
QY 145 ISTNKTVTVAQETDLKVRFLTAQHLQYSSGSSYKSGRLVFTHTNDNSDKYSFDFLYVGYR 204
Db 121 ISTNKTVTVAQETDLKVRFLTAQHLQYSSGSSYKSGRLVFTHTNDNSDKYSFDFLYVGYR 180
QY 205 DKESIFKVKYKDNKSFNIDKIGHLDIEIDS 233
Db 181 DKESIFKVKYKDNKSFNIDKIGHLDIEIDS 209

RESULT 8
Q9LAE1 PRELIMINARY; PRT; 209 AA.
AC Q9LAE1
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE Mitogenic exotoxin 2-3 (Fragment).
GN SMEZ-3.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=11681.
RX MEDLINE=20273982; PubMed=10811869;
RA Proft T., Mofatt S.L., Weller K.D., Paterson A., Martin D.,
RA Fraser J.D.;
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
RT Mosaic Structure, and Significant Antigenic Variation.";
RL J. Exp. Med. 191:1765-1776(2000).
DR EMBL; AF143653; AAF66654.1; -.
DR HSSP; P13163; ISXT.
DR InterPro; IPR001961; Strep/Strep_toxin.
DR Pfam; PF01123; Strep_Strep_toxin; 1.
DR Pfam; PF02876; Strep_Strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER
SQ SEQUENCE 209 AA; 24071 MW; FDADFCD1AA87271 CRC64;

Query Match 88.1%; Score 1063; DB 2; Length 256;
Best Local Similarity 89.7%; Pred. No. 1.3e-70;
Matches 209; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

QY 1 MKTKLIFSFTSIFTAISRPFVGLVDNNSLLRNIIYTIYVEYSDIVDFKTSNHLVTK 60
Db 24 MKTKLIFSFTSIFTAISRPFVGLVDNNSLLRNIIYTIYVEYSDIVDFKTSNHLVTK 83
QY 61 KLDVDRDARDFINSEMEYAAANDFKTGKIAVSPFDWNLVSKGKVTAYTYGGITPYQK 120
Db 84 KLDVDRDARDFINSEMEYAAANDFKTGKIAVSPFDWNLVSKGKVTAYTYGGITPYQK 143
QY 121 TSIPKNIPVNLWNGKQISVPYNEISTNKTVTVAQETDLKVRFLTAQHLQYSSGSSYK 180
Db 144 LOYKLSLVYIGINRKQIPVYNQISPTKTTVAQETDLKVRFLTAQHLQYSSGSSYK 203
QY 181 GRVLFHTNDNSDKYSFDFLYVGYRDKESIFKVKYKDNKSFNIDKIGHLDIEIDS 233
Db 204 KGLVHTNDNSDKYSFDFLYVGYRDKESIFKVKYKDNKSFNIDKIGHLDIEIDS 256

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Query Match 88.3%; Score 1066; DB 2; Length 209;
Best Local Similarity 97.1%; Pred. No. 6.1e-71;
Matches 203; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 25 LEVDNNSLLRNIIYTIYVEYSDIVDFKTSNHLVTKKLDVDRDARDFINSEMEYAAANDF 84
Db 1 LEVDNNSLLRNIIYTIYVEYSDIVDFKTSNHLVTKKLDVDRDARDFINSEMEYAAANDF 60
QY 85 KTGDKIAVSPFDWNLVSKGKVTAYTYGGITPYQKTSIPKNIPVNLWNGKQISVPYNE 144
Db 61 KAGDKIAVSPFDWNLVSKGKVTAYTYGGITPYQKTSIPKNIPVNLWNGKQISVPYNE 120
QY 145 ISTNKTVTVAQETDLKVRFLTAQHLQYSSGSSYKSGRLVFTHTNDNSDKYSFDFLYVGYR 204
Db 121 ISTNKTVTVAQETDLKVRFLTAQHLQYSSGSSYKSGRLVFTHTNDNSDKYSFDFLYVGYR 180
QY 205 DKESIFKVKYKDNKSFNIDKIGHLDIEIDS 233
Db 181 DKESIFKVKYKDNKSFNIDKIGHLDIEIDS 209

RESULT 9
Q9X9R8 PRELIMINARY; PRT; 256 AA.
AC Q9X9R8
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DE 01-NAR-2002 (TREMBLrel. 20, Last annotation update)
DE SPEX-2 protein precursor.
GN SPEX.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=27195;
RA Gerlach D., Wagner M., Fleischer B., Schmidt K.H., Vettermann S.,
RA Reichardt W.;
RT "Biochemical purification and characterization of a basic superantigen
RT of Streptococcus pyogenes.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ243865; CAB51332.1; -.
DR HSSP; P13380; 1AN8.
DR InterPro; IPR001961; Strep/Strep_toxin.
DR Pfam; PF01123; Strep_Strep_toxin; 1.
DR Pfam; PF02876; Strep_Strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Signal.
FT SIGNAL.
FT SIGNAL.
SQ SEQUENCE 256 AA; 29608 MW; 17C82214D0D04FC7 CRC64;

Query Match 88.1%; Score 1063; DB 2; Length 256;
Best Local Similarity 89.7%; Pred. No. 1.3e-70;
Matches 209; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

QY 1 MKTKLIFSFTSIFTAISRPFVGLVDNNSLLRNIIYTIYVEYSDIVDFKTSNHLVTK 60
Db 24 MKTKLIFSFTSIFTAISRPFVGLVDNNSLLRNIIYTIYVEYSDIVDFKTSNHLVTK 83
QY 61 KLDVDRDARDFINSEMEYAAANDFKTGKIAVSPFDWNLVSKGKVTAYTYGGITPYQK 120
Db 84 KLDVDRDARDFINSEMEYAAANDFKTGKIAVSPFDWNLVSKGKVTAYTYGGITPYQK 143
QY 121 TSIPKNIPVNLWNGKQISVPYNEISTNKTVTVAQETDLKVRFLTAQHLQYSSGSSYK 180
Db 144 LOYKLSLVYIGINRKQIPVYNQISPTKTTVAQETDLKVRFLTAQHLQYSSGSSYK 203
QY 181 GRVLFHTNDNSDKYSFDFLYVGYRDKESIFKVKYKDNKSFNIDKIGHLDIEIDS 233
Db 204 KGLVHTNDNSDKYSFDFLYVGYRDKESIFKVKYKDNKSFNIDKIGHLDIEIDS 256

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QY 85 KTGDKIAVSPFDNNYLSKGVATYTGITPYQKTSIPKNIPVNLWINGKQISVPYNE 144
 Db 61 KAGDKIAVSPFDNNYLSKGVATYTGITPYQKTSIPKNIPVNLWINGKQISVPYNE 120
 QY 145 ISTNKTVTVAQETDLKVRKFLIAHQHLYSSGSSYKSGRLVFHTNDNSDKYSFDFLYVGYR 204
 Db 121 ISTNKTVTVAQETDLKVRKFLIAHQHLYSSGSSYKSGRLVFHTNDNSDKYSFDFLYVGYR 180
 QY 205 DKESIFKVKDKNSFNIDKIGHLDIEIDS 233
 Db 181 DKESIFKVKDKNSFNIDKIGHLDIEIDS 209

RESULT 13
 Q9SLH9 PRELIMINARY; PRT; 256 AA.
 AC Q9SLH9;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DE 01-MAY-2000 (TREMBlrel. 20, Last annotation update)
 GN SPEG.
 OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
 OC Streptococcaceae; Streptococcus.
 OX NCBI_TaxID=1314;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=27195;
 RX MEDLINE=20374978; PubMed=10913699;
 RA Gerlach D., Fleischer B., Wagner M., Schmidt K.H., Vettermann S.,
 RA Reichardt W.;
 RT "Purification and Biochemical Characterization of a Basic Superantigen
 RT (SPEG/SMEZ3)".
 RL PEMS Microbiol. Lett. 188:153-163(2000).
 DR EMBL; AJ243890; CAB51142.1; -;
 DR HSSP; P13380; IAN8.
 DR InterPro; IPR001961; Stap/Strep-toxin.
 DR Pfam; PF01123; Stap_Strp_toxin; 1.
 DR Pfam; PF02876; Stap_Strp_tox_C; 1.
 DR PRINTS; PR00279; BACTRLTOXIN.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 KW Signal.
 FT SIGNAL
 SQ SEQUENCE 256 AA; 29610 MW; 149E1774D0D04FC7 CRC64;

Query Match 87.7%; Score 1059; DB 2; Length 256;
 Best Local Similarity 89.3%; Pred. No. 2.5e-70;
 Matches 208; Conservative 5; Mismatches 20; Indels 0; Gaps 0;

QY 1 MKTKLIFGTSIFIAISRPFGLVDNNLLRNITYSTIVVEYSDIVDFKTSNHLVTK 60
 Db 24 MKTKLIFGTSIFIAISRPFGLVDNNLLRNITYSTIVVEYSDIVDFKTSNHLVTK 83
 QY 61 KLDVRDARDFINSEMDYANDFTKDGKIAVSPFDNNYLSKGVATYTGITPYQK 120
 Db 84 KLDVRDARDFINSEMDYANDFTKDGKIAVSPFDNNYLSKGVATYTGITPYQK 143
 QY 121 TSIPKNIPVNLWINGKQISVPYNEISTNKTVAQETDLKVRKFLIAHQHLYSSGSSYKS 180
 Db 144 LOYLKISLYIGINRKQIPVNPQISPTKTTVAQETDLKVRKFLIAHQHLYSSGSSYKS 203
 QY 181 GRLVHTNDNSDKYSFDFLYVGYRDKESIFKVKDKNSFNIDKIGHLDIEIDS 233
 Db 204 GKLVHTNDNSDKYSFDFLYVGYRDKESIFKVKDKNSFNIDKIGHLDIEIDS 256

RESULT 14
 Q9LAD1 PRELIMINARY; PRT; 209 AA.
 AC Q9LAD1;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Mitogenic exotoxin Z-14 (Fragment).
 GN SMEZ-14.
 OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
 OC Streptococcaceae; Streptococcus.
 OX NCBI_TaxID=1314;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=4202;
 RX MEDLINE=20273982; PubMed=10811869;
 RA Proft T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
 RA Fraser J.D.;
 RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
 RT Mosaic Structure, and Significant Antigenic Variation.";
 RL J. Exp. Med. 191:1765-1776(2000).
 DR EMBL; AF143664; AAF66664.1; -;
 DR HSSP; P13163; 1SXT.
 DR InterPro; IPR001961; Stap/Strep-toxin.
 DR Pfam; PF01123; Stap_Strp_toxin; 1.
 DR Pfam; PF02876; Stap_Strp_tox_C; 1.
 DR PRINTS; PR00279; BACTRLTOXIN.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 FT NON_TER
 SQ SEQUENCE 209 AA; 24122 MW; 0CF5D429E1B968FE CRC64;

Query Match 87.7%; Score 1058; DB 2; Length 209;
 Best Local Similarity 96.2%; Pred. No. 2.3e-70;
 Matches 201; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 25 LEVDNNSLLRNITYSTIVVEYSDIVDFKTSNHLVTKKLDVRDARDFINSEMDYANDF 84
 Db 1 LEVDNNSLLRNITYSTIVVEYSDIVDFKTSNHLVTKKLDVRDARDFINSEMDYANDF 60
 QY 85 KTGDKIAVSPFDNNYLSKGVATYTGITPYQKTSIPKNIPVNLWINGKQISVPYNE 144
 Db 61 KAGDKIAVSPFDNNYLSKGVATYTGITPYQKTSIPKNIPVNLWINGKQISVPYNE 120
 QY 145 ISTNKTVTVAQETDLKVRKFLIAHQHLYSSGSSYKSGRLVFHTNDNSDKYSFDFLYVGYR 204
 Db 121 ISTNKTVTVAQETDLKVRKFLIAHQHLYSSGSSYKSGRLVFHTNDNSDKYSFDFLYVGYR 180
 QY 205 DKESIFKVKDKNSFNIDKIGHLDIEIDS 233
 Db 181 DKESIFKVKDKNSFNIDKIGHLDIEIDS 209

RESULT 15
 Q9LAC7 PRELIMINARY; PRT; 209 AA.
 AC Q9LAC7;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DE Mitogenic exotoxin Z-18 (Fragment).
 GN SMEZ-18.
 OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
 OC Streptococcaceae; Streptococcus.
 OX NCBI_TaxID=1314;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=10763;
 RX MEDLINE=20273982; PubMed=10811869;
 RA Proft T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
 RA Fraser J.D.;
 RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
 RT Mosaic Structure, and Significant Antigenic Variation.";
 RL J. Exp. Med. 191:1765-1776(2000).
 DR EMBL; AF143668; AAF66668.1; -;
 DR HSSP; P13163; 1SXT.
 DR InterPro; IPR001961; Stap/Strep-toxin.

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DR Pfam: PF01123; Staph_Strp_toxin; 1.
DR Pfam: PF02876; Staph_Strp_tox_C; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 209 AA; 24214 MW; 5755ED7340D77527 CRC64;

Query Match      87.4%; Score 1055; DB 2; Length 209;
Best Local Similarity 96.2%; Pred.No. 3.9e-70;
Matches 201; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 25 LEVDNNSLLRNIVSTIVYISDIVIDFKTSHNLVTKLQVDRDARDFINSEMDIYAANDF 84
Db 1 LEVDNNSLLRNIVSTIVYISDIVIDFKTSHNLVTKLQVDRDARDFINSEMDIYAANDF 60

QY 85 KTGDKIAVSVFPDWNLYLSKGVATYTYGGITPYQKTSIPKNIPVNLWINGKQISVPYNE 144
Db 61 KTGDKIAVSVFPDWNLYLSKGVATYTYGGITPYQKTSIPKNIPVNLWINGKQISVPYNE 120

QY 145 ISTNKTITVTAQIDILKVRFLIAQHOLYSSGSSYKSGRLVFHTNDNSDKYSFDLFYVGYR 204
Db 121 ISTNKTITVTAQIDILKVRFLIAQHOLYSSGSSYKSGRLVFHTNDNSDKYSFDLFYVGYR 180

QY 205 DKESIFKYKDKNSNIDKIGHLDIIDS 233
Db 181 DKESIFKYKDKNSNIDKIGHLDIIDS 209

Search completed: February 14, 2003, 13:45:47
Job time : 36 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 14, 2003, 13:44:09 ; Search time 20 Seconds
(without alignments)
1119.966 Million cell updates/sec

Title: US-09-869-136-2
Perfect score: 1207
Sequence: 1 MKTKLIFSFTSIFIAISR.....KDNKSFNIDKIGHLDIEIDS 233

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR73:*

1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|-----------------------|
| 1 | 308 | 25.5 | 240 | 2 G89991 | extracellular ente |
| 2 | 297.5 | 24.6 | 242 | 2 C89969 | extracellular ente |
| 3 | 296 | 24.5 | 235 | 2 A30509 | exotoxin C precurs |
| 4 | 274 | 22.7 | 239 | 2 D89969 | enterotoxin SEM [i |
| 5 | 258.5 | 21.4 | 257 | 2 A28179 | enterotoxin E prec |
| 6 | 251.5 | 20.8 | 257 | 2 A28664 | enterotoxin A prec |
| 7 | 251 | 20.8 | 258 | 2 A33953 | enterotoxin D prec |
| 8 | 231 | 19.1 | 260 | 2 C89984 | enterotoxin P [imp |
| 9 | 210.5 | 17.4 | 236 | 2 S18789 | exotoxin A precurs |
| 10 | 199.5 | 16.5 | 236 | 2 S18786 | exotoxin type A pr |
| 11 | 196.5 | 16.3 | 236 | 2 S18783 | exotoxin type A pr |
| 12 | 195.5 | 16.2 | 251 | 1 S29559 | exotoxin type A pr |
| 13 | 194.5 | 16.1 | 260 | 2 S89969 | enterotoxin type A pr |
| 14 | 165.5 | 13.7 | 258 | 2 H89968 | enterotoxin Sen [i |
| 15 | 162.5 | 13.5 | 266 | 1 ENSAB6 | enterotoxin B prec |
| 16 | 161 | 13.3 | 258 | 2 G89968 | extracellular ente |
| 17 | 158 | 13.1 | 266 | 2 A60114 | enterotoxin C-2 pr |
| 18 | 156 | 12.9 | 266 | 2 S11885 | enterotoxin C3 - S |
| 19 | 153.5 | 12.7 | 286 | 1 ENSAC1 | enterotoxin C-1 pr |
| 20 | 132.5 | 11.0 | 136 | 2 A89969 | enterotoxin YENT2 |
| 21 | 122 | 10.1 | 250 | 1 A26152 | streptococcal pyro |
| 22 | 119 | 9.9 | 231 | 2 D89807 | exotoxin 11 [import |
| 23 | 118.5 | 9.8 | 292 | 2 A89807 | exotoxin 9 [import |
| 24 | 116.5 | 9.7 | 356 | 2 A89807 | exotoxin 8 [import |
| 25 | 113.5 | 9.4 | 234 | 2 B89992 | toxic shock syndro |
| 26 | 113 | 9.4 | 232 | 2 F89807 | exotoxin 13 [import |
| 27 | 112.5 | 9.3 | 234 | 1 XCSAS1 | toxic shock syndro |
| 28 | 110.5 | 9.2 | 4688 | 2 F82885 | hypothetical prote |
| 29 | 106.5 | 8.8 | 464 | 2 S44603 | C02F5.1 protein - |

| | | | | | |
|----|-------|-----|------|----------|---------------------|
| 30 | 106.5 | 8.8 | 594 | 2 A82913 | hypothetical prote |
| 31 | 104.5 | 8.7 | 241 | 2 B89888 | hypothetical prote |
| 32 | 103 | 8.5 | 1216 | 2 F84773 | protein F40H6.5 [i |
| 33 | 102.5 | 8.5 | 626 | 2 E82273 | accessory coloniza |
| 34 | 102 | 8.5 | 227 | 2 G89807 | exotoxin 14 [import |
| 35 | 102 | 8.5 | 540 | 2 T20352 | hypothetical prote |
| 36 | 102 | 8.5 | 963 | 2 C90535 | conserved hypotet |
| 37 | 100.5 | 8.3 | 532 | 2 G84931 | 60 kD inner-membra |
| 38 | 100.5 | 8.3 | 616 | 2 B90554 | lipoprotein [import |
| 39 | 100.5 | 8.3 | 631 | 2 C90552 | lipoprotein [import |
| 40 | 99.5 | 8.2 | 544 | 2 B81290 | hypothetical prote |
| 41 | 99 | 8.2 | 971 | 2 C82880 | conserved hypotet |
| 42 | 98.5 | 8.2 | 496 | 2 A81340 | probable periplasm |
| 43 | 98 | 8.1 | 1061 | 2 H90084 | hypothetical prote |
| 44 | 97.5 | 8.1 | 226 | 2 G89806 | exotoxin 6 [import |
| 45 | 97.5 | 8.1 | 860 | 2 T28227 | ORF MSV067 probabl |

ALIGNMENTS

RESULT 1

G89991
extracellular enterotoxin L [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C:Accession: G89991
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.;
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu,
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; PMID:21311952; PMID:11418146
A:Accession: G89991
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-240 <KUR>
A:Cross-references: GB:BA000018; PID:gl3701803; PIDN:BA843096.1; GSPDB:GN00149
A:Experimental source: strain N315
C:Genetics:
A:Gene: sel
C:Superfamily: enterotoxin B

| | | | | | |
|-----------------------|-----|--|-------------------------------------|--------|----------------|
| Query Match | | 25.5% | Score 308; | DB 2; | Length 240; |
| Best Local Similarity | | 33.5% | Pred. No. 1.5e-16; | | |
| Matches | | 83; | Conservative | 41; | Mismatches 96; |
| | | | | Indels | 28; |
| | | | | Gaps | 8; |
| QY | 1 | MKTKLIFSFTSIFIAISR | PVGLVDNNSLLRNIYTVVEYSDIVDFKTSNHLVTK | 60 | |
| DB | 1 | MKKRLLVIVITLFISSNHTVLSNGDVGPNLRFYTK--YEVNKL-NVKDKNSPESH | 57 | | |
| QY | 61 | KLDVRDARDFINSEMDVYANDFKTGKIAVSPFDNNYLSKGVTAITYGGITPYQ- | 119 | | |
| DB | 58 | RLEYSKNDTLVAEPDNEYITSDLK-GKNVDVFGIYKY----GSNRTYGGVTKAEN | 111 | | |
| QY | 120 | -KTSIPKNIPVNLWGKQISVYNEISTNKTVAQIDKRVKFLAQHQLYSSG--- | 175 | | |
| DB | 112 | NKLDSPRIIPINLIINGKHQVTTKSVSTDKKMTAQIDVYKRLQDENIYGHNDTG | 171 | | |
| QY | 176 | -----SSYKSRGLVFHNDNSDKYSFDLFYGVGRDKESIFKVKDNKSNFNDK | 223 | | |
| DB | 172 | KGKEYGTSKRYSGFDKGSVVFHMDGNS-FSYDLFTYGTGLPESFLIYKDNKTVDSQ | 230 | | |
| QY | 224 | IGHLDIEI | 231 | | |
| DB | 231 | F-HLDVEI | 237 | | |

RESULT 2

C89969
extracellular enterotoxin type I precursor [imported] - Staphylococcus aureus (stra
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001

C, superfamily: enterozoan 3

| | | | | |
|-----------------------|-------|---|----------------|---------------------|
| Query Match | 21.4% | Score 358.5 | DB 2 | Length 257; |
| Best Local Similarity | 26.4% | Pred. No. le-12; | | |
| Matches | 75; | Conservative 55; | Mismatches 67; | Indels 87; Gaps 13; |
| Qy | 1 | MKKTLLFSFISIFIA--IISRPVFG-----LEVDNSSL--LRNIY---37 | | |
| Db | 1 | MKKTAFIL--LLFIALTLTSPLVNGSEKSEINEKDLRKKSELORNALSNRLQIYYN57 | | |
| Qy | 38 | -----SIVIVE-----YSDIVDFKTSHNLVTKKLDVRDARDFFIN73 | | |
| Db | 58 | EKATENKESDDQFLNTLLFKGFFTGHPWYNDLLVD-----LGSKDATNKYKG106 | | |
| Qy | 74 | SEMDEYAANDFKTGDKIAVFSVPEDWNYLSKG---KVTAITYGGITPYQKTSI--PKNIP128 | | |
| Db | 107 | KKVDLYGAY-----YGYOCAGGTPNKTCACHYGGVTLHDNNRLTEEEKVP150 | | |
| Qy | 129 | VNLWNGKQISVPYNEISTNKTVTTAQSIDLKVKRFELTAQHQLYSS---GSSYKSGRLVF185 | | |
| Db | 151 | INLWIDGKQTVPIIDKYKTSKEVTQVELDIQAARHYLHGKFGTLNDSFSGKVGQGLIVF210 | | |
| Qy | 186 | HTNDNSDKYSFDLPYVGVYRDKESIFKYVKDNKSPNIDKIGHLDI229. | | |
| Db | 211 | HSSEGS--TVSYDLFDACQYDPTLLRIYRDNKTINSENL-HIDL252 | | |

RESULT 6
A:Z88664
 enterotoxin A precursor - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 15-Oct-1999
C:Accession: A28664; A29566
R:Betley, M.J.; Mekalanos, J.J.
J. Bacteriol. 170, 34-41, 1988
A:Title: Nucleotide sequence of the type A staphylococcal enterotoxin gene.
A:Reference number: A28664; UID:88086892; PMID:3335483
A:Accession: A28664
A:Molecule type: DNA
A:Residues: 1-257 <BET>
A:Cross-references: GB:U18970; UID:gl53120; PIDN:AAA26681.1; PID:gl53121
A:Experimental source: strain FRI37
R:Huang, I.Y.; Hughes, J.L.; Bergdoll, M.S.; Schantz, E.J.
J. Biol. Chem. 262, 7006-7013, 1987
A:Title: Complete amino acid sequence of staphylococcal enterotoxin A.
A:Reference number: A29566; UID:87222293; PMID:3584106
A:Accession: A29566
A:Molecule type: protein
A:Residues: 25-241, 'S', 243-257 <HUA>
C:Genetics:
A:Gene: entA
A:Map position: 6
C:Superfamily: enterotoxin B

[illegible]

RESULT 7
A33953
enterotoxin D precursor - *Staphylococcus aureus*
C:Species: *Staphylococcus aureus*
C:Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 15-Oct-1999
C:Accession: A33953
R:Bayles, K.W.; Tandolo, J.J.
J. Bacteriol. 171, 4799-4806, 1989
A:Title: Genetic and molecular analyses of the gene encoding staphylococcal enterotoxin
A:Reference number: A33953; MUID:89359112; PMID:2549000
A:Accession: A33953
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-258 <BAY>
A:Cross-references: GB:M28521; NID:g1492109; PIDN:AA806195.1; PID:g758691
C:Superfamily: enterotoxin B

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Query Match      20.8%; Score 251; DB 2; Length 258;
Best Local Similarity 29.4%; Pred. No. 3.8e-13;
Matches 77; Conservative 57; Mismatches 86; Indels 42; Gaps 13;

QY    1 MKKTKLIFS---FWSIFATILSRPVGLEVDNN-----SLLRNIVSTIYYEY 44
      ||| : : ||| : : : : | : : | : : | : : |
Db    1 MKKENILALFFTSVLISPLN----VKANENIDSVKEKELHKSELSALNMKHSY 55

QY    45 SD---IVIDEFTS-----HNLVTKKL--DYRDARDPFINSEMDEYAANDFKTGDKIAVF 93
      : : | : | : : : : : : : | : : | : : | : : |
Db    56 ADKNPIIGENKSGDGFLENLTLLKKFTFDLINFEEDLLINFNSKEMAQH--PKS-KNVDDY 113

QY    94 SVFPEDWN--YLSSGKVTAITYTGGITPYO--KTSIPKNTPVNLWINGKOISVPYNISTNKT 150
      : : : : | ||| : ||| : : | : | : | : | : : | : : |
Db    114 PIRYSINCYGGEIDRTACTYGGVTPEHGKULKERRKLPINLWINGVQEVSLDKVOTDKK 173

QY    151 TVTAQEIDLKVRKELLIAHQHLYSS---GSSYKSGLRVFHETNDNSDKYSFDLFYVGYRDK 207
      ||| : : | : | : : : : : : : | : : | : : | : : |
Db    174 NVTVOELDAQARRYLRQLDKLYNNDTLGGKIQRKIEPDSDDGS-KVSYDLDFKVGDPPE 232

QY    208 SIFKYVDKNSFNIDKIGHLDI 229
      : : | ||| : : : | |||
Db    233 KQLRIYSDNKTLSTEHL-HIDI 253

```

RESULT 8
 C89984
 enterotoxin P [imported] - *Staphylococcus aureus* (strain N315)
 C:Species: *Staphylococcus aureus*
 C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
 C:Accession: C89984
 C:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cul-
 ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Seki-
 C: Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
 Lancet 357, 1225-1240, 2001
 A:Title: Whole genome sequencing of *meticillin*^R-resistant *Staphylococcus aureus*.
 A:Reference number: A89758; PMID:2131952; PMID:11418146
 A:Accession: C89984
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-260 <KUR>
 A:Cross-references: GB:BA000018; PID:gl3701743; PIDN:BAW43036.1; GSPDB:GN00149
 A:Experimental source: strain N315
 C:Genetics:
 C:Superfamily: enterotoxin B
 Query Match 19.1% Score 231; DB 2; Length 260;
 Best Local Similarity 28.1%; Pred. No. 1.3e-10;
 Matches 73; Conservative 48; Mismatches 97; Indels 42; Gaps 13

```
QY 2 KTKLIFSTSFIAISR-----VFGLEYDNN-----LLRNIYSTIWEYSD 46
  | | : | | : | : | : | : | : | : | : | : | : | : | : | : |
Db 6 KTTFILLSP--IALTITSPVNCSEKSEINGKDLQKSELOGTALSNLRQT-YYHNGS 62
```

QY 47 IVIDPKTSHNLVTKKLDVRDARDFINSEM-----DEYAANDFKTGKIAVFSVPF 97
Db 63 ALIENKESNDQFLKNTIL--FNDFFTGHQWYNDLLVDLGSKDTANIYK-GKKVDLYGVY 119
QY 98 DNNYLSKGV---TAYTGGITPYOKTSI--PKNTIPVNLWINGKQISVYPYNEISNKTIV 152
Db 120 --GYOCTGTPKTKACMTGGVTLHDNNQLEEKVPIINLWDGKONTVPLGFPVKTKREV 177
QY 153 TAEIDLKVRLIAHQHLYSS--GSSVKSGLRVFHTNDNSDKYSFDFLYGVYGRDKESI 209
Db 178 TVQELDLSRHLVHTYNYLNTDAFNGRIQRLIEFHPIS-SGDSVGYDLFGAQQGYPTQ 236
QY 210 FKVKDNKSNFNTDKIGHLDI 229
Db 237 LRIYRDNKTIK-SKNHIDI 255

RESULT 9
S18789
exotoxin A precursor (allele 4) - Streptococcus pyogenes (strain MGAS262 isolate California)
N:Alternate names: scarlet fever toxin
C:Species: Streptococcus pyogenes
A:Variety: strain MGAS262 isolate California
C:Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 16-Jul-1999
C:Accession: S18789
J. Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
J. Exp. Med. 174, 1271-1274, 1991
A:Title: Characterization and clonal distribution of four alleles of the *speA* gene
A:Reference number: S18782; MUID:92044323; PMID:1940804
A:Accession: S18789
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NE>
A:Cross-references: EMBL:X61563; NID:947303; PIDN:CAA43771.1; PID:947304
A:Experimental source: strain MGAS262 isolate California
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
C:Genetics:
A:Gene: *speA*
C:Superfamily: enterotoxin B
C:Keywords: exotoxin
F:1-22/Domain: signal sequence (fragment) #status predicted <SIG>
F:23-236/Product: exotoxin A (fragment) #status predicted <MAT>

Query Match 17.4%; Score 210.5; DB 2; Length 236;
Best Local Similarity 29.4%; Pred. No. 4.5e-09;
Matches 73; Conservative 47; Mismatches 77; Indels 51; Gaps 13;

QY 5 KLIFSFTSIFIAI-ISRPFVGLVDNNSL-----LRNIYSTIVVEYSDIV----- 48
Db 2 KIVFVLAIFLGLTTSQEVFAQQDPNPQLHRSSLVKLNQIY--FLYEGDPVWHENKVS 59
QY 49 IDFKTSHNLV-----TKKLDVRDARDFINSEMDEYAANDFKTGKIAVFSVPF 97
Db 60 VDQLLSHLIYNVSLNVDKLTTELKNEKSTLTKKNVD-----IYGEY 105
QY 98 DWN-YLSK-GKVTAYTGGITPYO--KTSIPKNTIPVNLWINGKQISVYPYNEISNKTIV 153
Db 106 YHCHYLCNARRACIYGGVTNHEGNHLEIPKILNVLKSIDGIQ-SLSF-DIETSKKMT 163
QY 154 AQEIDLKVRLIAHQHLYSS--SSYKSGRLVFTNDNSDKYSFDFLYGVYGRDKESIFKV 212
Db 164 AQEIDYKVRKHLTNKQITNGSPKIETGYIKFISKD-KETFWDFDFPEPEFNQVYLM 222
QY 213 YKDNKSN 220
Db 223 YKDNETLD 230

RESULT 10
S18786
exotoxin type A precursor (allele 2) - Streptococcus pyogenes phage (strain MGAS250 isolate California)
N:Alternate names: scarlet fever toxin
C:Species: Streptococcus pyogenes phage
A:Variety: strain MGAS250 isolate California; strain MGAS251 isolate California; strain

isolate United Kingdom; strain MGAS496 isolate Germany
C:Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 16-Jul-1999
C:Accession: S18786; S18787; S18788; S18790; S18792; S18795; S18799
J. Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
J. Exp. Med. 174, 1271-1274, 1991
A:Title: Characterization and clonal distribution of four alleles of the *speA* gene
A:Reference number: S18782; MUID:92044323; PMID:1940804
A:Accession: S18786
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NE>
A:Cross-references: EMBL:X61561; NID:947297; PIDN:CAA43759.1; PID:947298
A:Experimental source: strain MGAS250 isolate California unassigned phage
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
C:Genetics:
A:Gene: *speA2*
C:Superfamily: enterotoxin B
C:Keywords: exotoxin
F:1-22/Domain: signal sequence (fragment) #status predicted <SIG>
F:23-236/Product: exotoxin type A (fragment) #status predicted <MAT>

Query Match 16.5%; Score 199.5; DB 2; Length 236;
Best Local Similarity 30.2%; Pred. No. 3.1e-08;
Matches 74; Conservative 48; Mismatches 78; Indels 45; Gaps 16;

QY 5 KLIFSFTSIFIAI-ISRPFVGLVDNNSLNRNIYSTIVVEYSDIV-----ID 50
Db 2 KIVFVLAIFLGLTTSQEVFAQQDPNPQLHRSSLVKLNQIYFLYEGDPVWHENKVS 61
QY 51 FKTSNHLVTK-----KLDVRDARDFINSEMDEYAANDFKTGDK-IAVFSVP-FDW 99

| | | | |
|---|---|---|--|
| Db | 62 | QLLSDLLIYVNGPNVDKLTTELK-----NQEM---- | -ATLFK--DKNIDIVSVEYYHL 108 |
| Qy | 100 | NYL-SKGKTAVTYGGITPYO--KTSIPKNIPVNLMWINGKOISVPNEISTNKTVTAAQE 156 | |
| Db | 109 | CYLENAERSACIIYGTVNHGHNLEPKKIIVKVYSIDIGIQ-SLSF-DIETNNKKWTAAQE 166 | |
| Qy | 157 | IDLVKRFLTAQHLYSSG-SSYKSGLRVFHNTNDNSDKYSFDLPFYGVYRKESIFKYVKD 215 | |
| Db | 167 | L DYKVRKYLTDNKOLYTNGPSKYTGVIKF-I PKNKSEFWDFEFPPEPTQSXYLI MYKD 225 | |
| Qy | 216 | NKSFN 220 | |
| Db | 226 | NETLD 230 | |
| RESULT 11 | | | |
| S18783 | exotoxin type A precursor (allele 3) - Streptococcus pyogenes phage (strain MGAS158 isolate) | | |
| N: | Alternate names: scarlet fever toxin | | |
| C: | Species: Streptococcus pyogenes phage | | |
| A: | Variety: strain MGAS158 isolate Nebraska; strain MGAS485 isolate Yugoslavia; strain MGAS158 isolate Nebraska; #sequence_revision 29-Jan-1993 #text_change 16-Jul-1999 | | |
| C: | Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 16-Jul-1999 | | |
| C: | Accession: S18783; S18793; S18794; S18801; S18798 | | |
| R: | Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M. | | |
| J: | Exp. Med. 174, 1271-1274, 1991 | | |
| A: | Title: Characterization and clonal distribution of four alleles of the speA gene encoded by streptococcus pyogenes | | |
| A: | Reference number: S18782; MUID:92044323; PMID:1940804 | | |
| A: | Status: nucleic acid sequence not shown; translation not shown | | |
| A: | Molecule type: DNA | | |
| A: | Residues: 1-236 <NEL> | | |
| A: | Cross-references: EMBL:X61568; NID:g47289; PIDN:CAA43766.1; PID:g47290 | | |
| A: | Experimental source: strain MGAS158 isolate Nebraska unassigned phase | | |
| A: | Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991 | | |
| A: | Accession: S18793 | | |
| A: | Status: nucleic acid sequence not shown; translation not shown | | |
| A: | Molecule type: DNA | | |
| A: | Residues: 1-236 <NEA> | | |
| A: | Cross-references: EMBL:X61569; NID:g47313; PIDN:CAA43767.1; PID:g47314 | | |
| A: | Experimental source: strain MGAS485 isolate Yugoslavia unassigned phase | | |
| A: | Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991 | | |
| A: | Accession: S18794 | | |
| A: | Status: nucleic acid sequence not shown; translation not shown | | |
| A: | Molecule type: DNA | | |
| A: | Residues: 1-236 <NEZ> | | |
| A: | Cross-references: EMBL:X61570; NID:g47315; PIDN:CAA43768.1; PID:g47316 | | |
| A: | Experimental source: strain MGAS491 isolate United Kingdom unassigned phase | | |
| A: | Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991 | | |
| A: | Accession: S18801 | | |
| A: | Status: nucleic acid sequence not shown; translation not shown | | |
| A: | Molecule type: DNA | | |
| A: | Residues: 1-236 <NEY> | | |
| A: | Cross-references: EMBL:X61572; NID:g47333; PIDN:CAA43770.1; PID:g47334 | | |
| A: | Experimental source: strain MGAS624 isolate Germany unassigned phase | | |
| A: | Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991 | | |
| A: | Accession: S18798 | | |
| A: | Status: nucleic acid sequence not shown; translation not shown | | |
| A: | Molecule type: DNA | | |
| A: | Residues: 1-236 <NEO> | | |
| A: | Cross-references: EMBL:X61571; NID:g47323; PIDN:CAA43769.1; PID:g47324 | | |
| A: | Experimental source: strain MGAS495 isolate Germany unassigned phase | | |
| A: | Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991 | | |
| C: | Genetics: | | |
| G: | Gene: speA3 | | |
| C: | Superfamily: enterotoxin B | | |
| K: | Keywords: exotoxin | | |
| F: | 1-23/Domain: signal sequence (fragment) #status predicted <SIG> | | |
| F: | 23/23/Product: exotoxin type A (fragment) #status predicted <MAT> | | |
| Query Match 16.3%; Score 196.5; DB 2; Length 236; | | | |
| Best Local Similarity 30.2%; Pred. No. 5.3e-08; | | | |
| Matches | 74; | Conservative | 47; Mismatches 79; Indels 45; Gaps 16; |

```

Qy 29 NNSLLRNLYSTI-----VVEYSDIVDFKTSNHLVTKKLDVRDARDFINSEMDEYAAN 82
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 53 NDDYINRRFTTVKSVISTTEKFLDFDLFSINWLGDIGISNEFKDLKVESSAI-----SK 108
Qy 83 DFKTGDKIAVESPFDDNNYLSKGKV-TAYTYGGITPYQ--KTSIPKNIPVNLWINGKQIS 139
   | : | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 109 EF-LGKTVDIYGVYKAHCHGEHQVDTACTYGGVTPHENKNLSEPKNIGVAVKD--NVN 165
Qy 140 VPYNEISTNKTVTYTAQIEDLKVKRFLAQHOLYS-SGSSVKSRLVFHT--NNSDKYSFD 197
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 166 VNTFIVTDDKKVTAQELDKVTRTKUNNAYKLYDRMTSDVQKGVIKFSHSEKSESFYD 225
Qy 198 LFYGYGRDKESIFKVVYKDNKSFNDKIGHLDI 229
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 226 LFYIKGNLPDQYLQIYNDNKTIDSSDY-HIDV 256

RESULT 14
H89968
enterotoxin SEN [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C:Accession: H89968
R:Kuroda, M.; Ohca, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.;
ma, A.; Mizutani-Uji, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aur
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: H89968
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-258 <KUR>
A:Cross-references: GB:BA000018; PID:g13701618; PIDN:BA842911.1; GSPDB:GN0
A:Experimental source: strain N315
C:Genetics:
A:Gene: sen
C:Superfamily: enterotoxin B

Query Match 13.7%; Score 165.5; DB 2; Length 258;
Best Local Similarity 25.6%; Pred. No. 1.4e-05;
Matches 66; Conservative 53; Mismatches 102; Indels 37; Gaps

Qy 1 MKKTKLIFSFTSIFI---AISRPFVGLVEDNNSL-----LRNIYSTIVY-- 42
   | : | : : : : : : : : : : : : : : : : : : : : : : : :
Db 4 IKKLMLRFYAAIIITLLCLINNNYNAEVDKDLAKKSLDSSKFLNLTSYTDTITWOL 63
Qy 43 -EYSDIVIDFKTSNHLVTKKLDVRDARDFINSEMDEY-AANDFKTGDKIAVESYPPFDWN 100
   | : : : : : : : : : : : : : : : : : : : : : : : : :
Db 64 DESNKISTDQLLNTIILKNIDISVLKTSLSKVEFNSSDLANQFK-GKNIDIYGLYFGNK 122
Qy 101 Y--LSGKVTAYTYGGITPYQKTSI--PKNIPVNLWINGKQISVPYNE---ISTWKTVT 153
   | : : : : : : : : : : : : : : : : : : : : : : : : :
Db 123 CVGLTEEK-TCSLYGGVTHDGNQLDEERVIGNVFVKDGVQ-----QEGFVIKTKKAVT 176
Qy 154 AQEIDLKVKRFLAQHOLYS-SGSSVKSRLVFHTNDSDK-YSPDLFVGVYDRKESIFK 211
   | : : : : : : : : : : : : : : : : : : : : : : : : :
Db 177 VQELDTKVRKLENLKIYNTKDGNIQKGIFFHSHNHODQSFYDLYNVKSGVGAEEFFQ 236
Qy 212 VYKDNKSFNDKIGHLDI 229
   | : : : : : : : : : : : : : : : : : : : : : : : : :
Db 237 FYSNRTVSSNY-HIDV 253

RESULT 15
ENSAB6
enterotoxin B precursor - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 24-Apr-1984 #sequence_revision 15-Oct-1996 #text_change 18-Jun-1998
C:Accession: S27360; A92065; S27240; A01815
R:Jones, C.L.; Khan, S.A.
J. Bacteriol. 166, 29-33, 1986

```

Search completed: February 14, 2003, 13:46:12
Job time : 21 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 14, 2003, 13:44:04 ; Search time 12 seconds

(without alignments)

805.332 Million cell updates/sec

Title: US-09-869-136-2

Perfect score: 1207

Sequence: 1 MKYTKLIFSTSFIAISR.....KDNKSPNIDKIGHLDIEIDS 233

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1 | 305 | 25.3 | 235 | 1 | SPEC_STRPY |
| 2 | 258.5 | 21.4 | 257 | 1 | ETXE_STAAU |
| 3 | 251.5 | 20.8 | 257 | 1 | ETXA_STAAW |
| 4 | 251 | 20.8 | 258 | 1 | ETXD_STAAU |
| 5 | 243 | 20.1 | 234 | 1 | SPEC_STRPY |
| 6 | 203 | 16.8 | 236 | 1 | SPEH_STRPY |
| 7 | 195.5 | 16.2 | 251 | 1 | SPEA_STRPY |
| 8 | 162.5 | 13.5 | 266 | 1 | ETXB_STAAU |
| 9 | 161 | 13.3 | 258 | 1 | ETXC_STAAU |
| 10 | 158 | 13.1 | 266 | 1 | ETC2_STAAU |
| 11 | 156 | 12.9 | 266 | 1 | ETC3_STAAU |
| 12 | 153.5 | 12.7 | 266 | 1 | ETC1_STAAU |
| 13 | 112.5 | 9.3 | 234 | 1 | TSTT_STAAU |
| 14 | 106.5 | 8.8 | 1010 | 1 | YK11_CAEEL |
| 15 | 103 | 8.5 | 1216 | 1 | YK11_CAEEL |
| 16 | 100.5 | 8.3 | 532 | 1 | 60IN_BUCAI |
| 17 | 93.5 | 7.7 | 444 | 1 | TIG_MYCPN |
| 18 | 93 | 7.7 | 691 | 1 | LCN3_LACLA |
| 19 | 93 | 7.7 | 823 | 1 | AXL2_YEAST |
| 20 | 91.5 | 7.6 | 645 | 1 | REP_BUCAI |
| 21 | 91 | 7.5 | 380 | 1 | RMAR_WILMR |
| 22 | 91 | 7.5 | 386 | 1 | VC17_VACCC |
| 23 | 91 | 7.5 | 760 | 1 | ETF2_MSEPV |
| 24 | 88 | 7.3 | 667 | 1 | Y366_MYCGE |
| 25 | 87.5 | 7.2 | 602 | 1 | EXSA_BUCAI |
| 26 | 87.5 | 7.2 | 1155 | 1 | IFP2_METJA |
| 27 | 87.5 | 7.2 | 1276 | 1 | BXD_CLOBO |
| 28 | 87 | 7.2 | 540 | 1 | MTA1_ACICA |
| 29 | 86.5 | 7.2 | 590 | 1 | MSP_TRELE |
| 30 | 86.5 | 7.2 | 905 | 1 | YD83_HUMAN |
| 31 | 86 | 7.1 | 415 | 1 | CC11_YEAST |
| 32 | 86 | 7.1 | 1616 | 1 | SLAP_BACCI |
| 33 | 86 | 7.1 | 3744 | 1 | YHP9_YEAST |

ALIGNMENTS

RESULT 1

| ID | SPEC_STRPY | STANDARD; | PRT; | 235 AA. |
|----|--|-----------|------|---------|
| DT | 01-JAN-1990 (Rel. 13, Created) | | | |
| DT | 16-OCT-2001 (Rel. 40, Last sequence update) | | | |
| DT | 16-OCT-2001 (Rel. 40, Last annotation update) | | | |
| DE | Exotoxin type C precursor (SPE C). | | | |
| GN | SPEC OR SPY0711. | | | |
| OS | Streptococcus pyogenes. | | | |
| OC | Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; | | | |
| OC | Streptococcus. | | | |
| OX | NCBI_TaxID=1314; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A., AND SEQUENCE OF 28-52. | | | |
| RC | SERAIN-118P / MGAS 1501 | | | |
| RC | MEDLINE-92363541; PubMed=1564157. | | | |
| RA | Kapur V., Nelson K., Schlievert P.M., Selander R.K., Musser J.M.; | | | |
| RT | "Molecular population genetic evidence of horizontal spread of two | | | |
| RT | alleles of the pyrogenic exotoxin C gene (speC) among pathogenic | | | |
| RT | clones of Streptococcus pyogenes." | | | |
| RL | Infect. Immun. 60:3513-3517(1992). | | | |
| RN | [3] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | STRAIN-SF370 / ATCC 700294 / Serotype M1; | | | |
| RC | MEDLINE-21192684; PubMed=11296296; | | | |
| RA | Ferretti J.J., McShan W.M., Aldic D.J., Savic D.J., Savic G., Lyon K., | | | |
| RA | Primeaux C., Szentei S., Savorov A.N., Kanton S., Lai H.S., Lin S.P., | | | |
| RA | Qian X., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J., | | | |
| RT | Yuan X., Clifton S.W., Roe B.A., McLaughlin R.; | | | |
| RT | "Complete genome sequence of an M1 strain of Streptococcus | | | |
| RT | pyogenes." | | | |
| RL | Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001). | | | |
| RN | [4] | | | |
| RP | X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 30-215 | | | |
| RC | MEDLINE-97397332; PubMed=9253413; | | | |
| RA | Roussel A., Anderson A.F., Baker H.M., Fraser J.D., Baker E.N.; | | | |
| RT | "Crystal structure of the streptococcal superantigen SPE-C: | | | |
| RT | dimerization and zinc binding suggest a novel mode of interaction | | | |
| RT | with MHC class II molecules." | | | |
| RL | Nat. Struct. Biol. 4:635-643(1997). | | | |
| CC | -I- SUBUNIT: Binds to major histocompatibility complex class II beta | | | |
| CC | chain. | | | |
| CC | -I- DISEASE: THE STREPTOCOCCAL PYROGENIC TOXINS A, B, AND C ARE | | | |
| CC | THE CAUSATIVE AGENTS OF THE SYMPTOMS ASSOCIATED WITH SCARLET | | | |
| CC | FEVER, HAVE BEEN ASSOCIATED WITH STREPTOCOCCAL TOXIC SHOCK-LIKE | | | |
| CC | DISEASE AND MAY PLAY A ROLE IN THE EARLY EVENTS OF RHEUMATIC | | | |
| CC | FEVER. | | | |
| CC | -I- MISCELLANEOUS: THIS TOXIN SEEMS TO BE CODED BY A BACTERIOPHAGE. | | | |

| | | | | | |
|----|------|-----|------|---|------------|
| 34 | 85.5 | 7.1 | 530 | 1 | TP6B_SULSO |
| 35 | 85.5 | 7.1 | 997 | 1 | T257_ECOLI |
| 36 | 85 | 7.0 | 303 | 1 | Y114_MERJA |
| 37 | 85 | 7.0 | 617 | 1 | Y237_BUCAI |
| 38 | 85 | 7.0 | 1085 | 1 | IFH1_YEAST |
| 39 | 84.5 | 7.0 | 335 | 1 | Y063_BORBU |
| 40 | 84.5 | 7.0 | 413 | 1 | Y071_MYCNY |
| 41 | 84.5 | 7.0 | 428 | 1 | G6P1_MYGGA |
| 42 | 84.5 | 7.0 | 841 | 1 | PSPI_YEAST |
| 43 | 84 | 7.0 | 970 | 1 | Y087_BUCAI |
| 44 | 84 | 7.0 | 1157 | 1 | C8AA_BACUK |
| 45 | 83.5 | 6.9 | 1901 | 1 | YCF1_TOBAC |

| | |
|--------|-------------|
| Q972f0 | sulfolobus |
| P25239 | escherichia |
| Q57578 | methanococc |
| P57331 | buchnera ap |
| P39520 | saccharomyc |
| O51090 | borrelia bu |
| P5802 | mycoplasma |
| Q6x58 | mycoplasma |
| P50896 | saccharomyc |
| P37189 | buchnera ap |
| Q45704 | bacillus th |
| P12222 | nicotiana t |

DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Enterotoxin type A precursor (SEA).
 GN ENTA OR MW1889.
 OS Staphylococcus aureus (strain MW2), and
 OC Staphylococcus aureus.
 CC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=196620, 1280;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-MW2;
 RX MEDLINE=22040717; PubMed=12044378;
 RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
 RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
 RA Yanamoto K., Hiramatsu K.;
 RT "Genome and virulence determinants of high virulence community-
 RT acquired MRSA";
 RL Lancet 359:1819-1827(2002).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN-FRI337;
 RX MEDLINE=88086892; PubMed=3335483;
 RA Betley M.J., Mekalanos J.J.;
 RT "Nucleotide sequence of the type A staphylococcal enterotoxin gene";
 RL J. Bacteriol. 170:34-41(1988).
 RN (3)
 RP SEQUENCE OF 25-257.
 RX MEDLINE=87222293; PubMed=3584106;
 RA Huang I.-Y., Hughes J.L., Bergdoll M.S., Schantz E.J.;
 RT "Complete amino acid sequence of staphylococcal enterotoxin A";
 RL J. Biol. Chem. 262:7006-7013(1987).
 RN (4)
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX MEDLINE=95354648; PubMed=7628431;
 RA Schad E.M., Zaitseva I., Zaitsev V.N., Dohlsten M., Kalland T.,
 RA Schlievert P.M., Ohlendorf D.H., Svensson L.A.;
 RT "Crystal structure of the superantigen staphylococcal enterotoxin
 RT type A";
 RL EMBO J. 14:3292-3301(1995).
 RN (5)
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
 RX MEDLINE=97113025; PubMed=8943278;
 RA Sundstroem M., Hallen D., Svensson A., Schad E., Dohlsten M.,
 RA Abrahmsen L.;
 RT "The Co-crystal structure of staphylococcal enterotoxin type A with
 RT Zn2+ at 2.7-A resolution. Implications for major histocompatibility
 RT complex class II binding";
 RL J. Biol. Chem. 271:32212-32216(1996).
 RN (6)
 RP 3D-STRUCTURE MODELING.
 RX MEDLINE=96022987; PubMed=7552730;
 RA Swaminathan S., Furey W.F. Jr., Pletcher J., Sax M.;
 RT "Residues defining V beta specificity in staphylococcal
 RT enterotoxins";
 RL Nat. Struct. Biol. 2:680-686(1995).
 RN (7)
 RP COMPARISON OF STRUCTURE OF SEA AND SEC2.
 RX MEDLINE=97334373; PubMed=9191070;
 RA Schad E.M., Papageorgiou A.C., Svensson L.A., Acharya K.R.;
 RT "A structural and functional comparison of staphylococcal
 RT enterotoxins A and C2 reveals remarkable similarity and
 RT dissimilarity";
 RL J. Mol. Biol. 269:270-280(1997).
 CC -1- COFACTOR: Binds 1 zinc ion per subunit. The zinc ion is necessary
 CC for the toxin interaction with MHC class II.
 CC -1- SUBUNIT: MONOMER.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
 CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
 CC -1- MISCELLANEOUS: THIS TOXIN SEEMS TO BE CODED BY A BACTERIOPHAGE.
 CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
 CC FAMILY.
 CC -----
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 CC -----
 DR EMBL; AP004828; BAB95754.1; -
 DR EMBL; M18970; AAA26681.1; -
 DR PIR; A28664; A28664.
 DR PIR; A29566; A29566.
 DR PDB; IESF; 1I-JUL-96.
 DR PDB; ISEA; 15-OCT-95.
 DR PDB; 1SXT; 19-NOV-97.
 DR InterPro; IPR001961; Staph/Strep_toxin.
 DR Pfam; PF01123; Staph_Strep_toxin_1;
 DR Pfam; PF02876; Staph_Strep_toxin_C_1;
 DR PRINTS; PR00279; BACTRLTOXIN.
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1;
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2;
 KW Enterotoxin; Toxin; Signal; Superantigen; Metal-binding; Zinc;
 KW 3D-structure.
 FT SIGNAL 1 24
 FT CHAIN 25 257 ENTEROTOXIN TYPE A.
 FT DISULFID 120 130
 FT METAL 211 211 ZINC.
 FT METAL 249 249 ZINC.
 FT METAL 251 251 ZINC.
 FT CONFLICT 242 242 T -> S (IN REF. 3).
 SQ SEQUENCE 257 AA; 29669 MW; ADEBF5BCALF14677 CRC64;
 Query Match 20.8%; Score 251.5; DB 1; Length 257;
 Best Local Similarity 29.9%; Pred. No. 4.6e-13;
 Matches 58; Conservative 40; Mismatches 59; Indels 37; Gaps 7;
 QY 44 YSDIVIDPKTSNLTVKLVDARDFFINSEMDYANDFTGDKIAVFSVPFQWNYLS 103
 DB 88 YNDLLVDF-----DSKDIVDKYKGVLDYGY- - - - - YGYQC 120
 QY 104 KG---KVTATYTGITPYQKTSI--PKNIPVNLWTNGKQISVPYNEISTNKTVTYTAQETD 158
 DB 121 AGGTGPNKACMGYVTLHDNNRLTEKKVPINLWLDGKQNTVPLETVTKNKNVTVQELD 180
 QY 159 LKVRFLIAHQOLYSS---GSSYKSGRLVFTNDNSDKYSFDFYVGVYGRDKESIFKVKYD 215
 DB 181 LQARRYLOEKYNLYNSVDVFGKVRGLIVFHTS-TEPSVNTYDLFGAQQGYSNTLLRIYRD 239
 QY 216 NKSFNIDKIGHLDI 229
 DB 240 NKTINSENN-HIDI 252
 RESULT 4
 ID ETXD_STAAU STANDARD; PRT; 258 AA.
 AC P20723;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Enterotoxin type D precursor (SED).
 GN ENTD.
 OS Staphylococcus aureus.
 CC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89359112; PubMed=2549000;
 RA Bayles K.W., Iandolo J.J.;
 RT "Genetic and molecular analyses of the gene encoding staphylococcal
 RT enterotoxin D";
 RL J. Bacteriol. 171:4799-4806(1989).
 RN (2)
 RP SEQUENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).

RC STRAIN-ATCC 23235;
 RX MEDLINE-97157473; PubMed-9003758;
 RA Sundstroem M., Abrahmsen L., Antonsson P., Mehindate K., Mourad W.,
 RA Dohlesten M.;
 RT "The crystal structure of staphylococcal enterotoxin type D reveals
 RT Zn2+-mediated homodimerization.";
 RL EMBO J. 15:6832-6840(1996).
 CC -1- SUBUNIT: HOMODIMER; ZINC-DEPENDENT.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
 CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
 CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
 CC FAMILY.
 CC
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 CC
 CC EMBL; M28521; AAB06195.1;
 DR PIR; A33953; A33953.
 DR HSP; P13163; ISXT.
 DR InterPro; IPR001961; Staph/Strep-toxin.
 DR Pfam; PF01123; Staph_strep_toxin; 1.
 DR Pfam; PF02876; Staph_strep_tox_C; 1.
 DR PRINTS; PR00279; BACTRLTOXIN.
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 KW Enterotoxin; Toxin; Signal; Superantigen; Zinc.
 FT SIGNAL 1 25
 FT CHAIN 26 258 ENTEROTOXIN TYPE D.
 FT METAL 212 212 ZINC.
 FT METAL 250 250 ZINC.
 FT METAL 252 252 ZINC.
 FT METAL 114 114 ZINC.
 FT VARIANT 114 114 P -> A (IN STRAIN ATCC 23235).
 SQ SEQUENCE 258 AA; 29746 MW; 4F7C6A28D42597FD CRC64;
 Query Match 20.8%; Score 251; DB 1; Length 258;
 Best Local Similarity 29.4%; Pred. No. 5.1e-13;
 Matches 77; Conservative 57; Mismatches 86; Indels 42; Gaps 13;
 QY 1 MKKTKLIFS---FTSIFTAISRVPVGLVDNN-----SLRLNIYSIVIEY 44
 DB 1 MKKFNILIALFTSLVISPLN-----VKANENIDSVKEKELHKKSELSTALNNKHSY 55
 QY 45 SD---IVDFKTS-----HNLVTKKL--DVRDARDFFINSEMDEYAANDFTGDKIAVF 93
 DB 56 ADKNPLIGENKSTGDOFLENTLLYKFFTDLINFEDLLINFNSKEMAGH-FKS-KNVDVY 113
 QY 94 SVPFOWN-YLSGKVTATYIGTIPYQ--KTSIPKNIPVNLWINGKQISVPYNEISTNKT 150
 DB 114 PIRYINCYGGIDFTACTYGGVTPHEGNKLERKIPINLWINGVQEVSLDKVOTDKK 173
 QY 151 TVTAGEIDLKVKRFLIAHQLYSS---GSSYKSGRLVFHTNDNSDKYSFDLFYVGYRKE 207
 DB 174 NVTQELDAQARYLQKDLKLYNNDTLGGKIQRGKIEFDSSDGS-KVSYDLFDVKGDPPE 232
 QY 208 SIFKYKKNKSNIDKIGHDI 229
 DB 233 KOLRIYDNKTLSTEHL-HIDI 253
 RESULT 5
 SPEG_STRPY STANDARD; PRT; 234 AA.
 AC Q9X5C7;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Exotoxin type G precursor (SPE G).

GN SPEG OR SPY0212.
 OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID-1314;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-M1;
 RX MEDLINE-99093428; PubMed-9874566;
 RA Proft T., Moffatt S.L., Berkahn C.J., Fraser J.D.;
 RT "Identification and characterization of novel superantigens from
 RT Streptococcus pyogenes.";
 RL J. Exp. Med. 189:89-102(1999).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN-SF370 / ATCC 700294 / Serotype M1;
 RX MEDLINE-21192684; PubMed-11296296;
 RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
 RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
 RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
 RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
 RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
 CC -1- SUBUNIT: Binds to major histocompatibility complex class II beta
 CC chain.
 CC -1- DISEASE: Mitogenic for human peripheral blood lymphocytes.
 CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
 CC FAMILY.
 CC
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 CC
 CC EMBL; AF134499; AAD30988.1;
 DR EMBL; AE006489; AAK33303.1;
 DR HSP; P13380; IAN8.
 DR InterPro; IPR001961; Staph/Strep-toxin.
 DR Pfam; PF01123; Staph_strep_toxin; 1.
 DR Pfam; PF02876; Staph_strep_tox_C; 1.
 DR PRINTS; PR00279; BACTRLTOXIN.
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; FALSE_NEG.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 KW Toxin; Signal; Complete proteome.
 FT SIGNAL 1 24 POTENTIAL.
 FT CHAIN 25 234 EXOTOXIN TYPE G.
 SQ SEQUENCE 234 AA; 27262 MW; 49525C49E4BA3052 CRC64;
 Query Match 20.1%; Score 243; DB 1; Length 234;
 Best Local Similarity 30.6%; Pred. No. 1.9e-12;
 Matches 72; Conservative 40; Mismatches 99; Indels 24; Gaps 8;
 QY 11 TSIFTAISRVPV---GLEV-----DNNSLRLNIYSIVIEYSIVIDEKTSNHLVTK 60
 DB 3 TNLITLILSCVFSGSLAYADENLKDLSRLRAYNTPCDYENVEFAVFTNSIHIN 62
 QY 61 KLDVARDARDFINSEMDEYAANDFTGDKIAVSPFDMN---YLSGKVTATYIGTIPY 118
 DB 63 TKQRSECLYVDSIVSLGITDQFIKDKVDVFGLPYNEPSPYVDN-----YGGIVKH 116
 QY 119 KTSIPKNIPVNLWIN--GKQISVPYNEISTNKTVTVAQIEDLKVKRFLIAHQLYSSGS 176
 DB 117 SNQG-NKSLQFVGLNODGKTYLPSEAVRIKKKQFTLQEFDFKIRKFLMEKYNIDSES 175
 QY 177 SYKSGRLVFHTNDNSDKYSFDLFYVGYR--DKESIFKYKKNKSNIDKIGHDI 229
 DB 176 RYTGSLFLATKD-SKHYEVDLNFKDDKLLSRDSEFFKRYKKNKIFNSEISHFDI 229
 RESULT 6

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SPEH_STRPY STANDARD; PRT; 236 AA.
ID Q9X5C8;
DT 16-OCT-2001 (Rel. 40, Created)
DD 16-OCT-2001 (Rel. 40, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
GN Exotoxin type H precursor (SPE H).
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M15;
RA Medline=99033428; PubMed=9874566;
RX Proft T., Moffatt S.L., Berkahn C.J., Fraser J.D.;
RT "Identification and characterization of novel superantigens from
RL Streptococcus pyogenes.";
RN J. Exp. Med. 189:89-102(1999).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=SF30 / ATCC 700294 / Serotype M1;
RX MEDLINE=21192684; PubMed=11296296;
RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
RL Proc. Natl Acad. Sci. U.S.A. 98:458-4663(2001).
CC -1- SUBUNIT: Bands to major histocompatibility complex class II beta
chain.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DISEASE: Mitogenic for human peripheral blood lymphocytes.
CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
FAMILY.
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EMBL; AF124500; AAC30989.1; .
DR EMBL; AE006546; AAK33907.1; .
DR HSSP; PL3163; 1SXT.
DR InterPro: IPR001961; Staph/Strep_toxin.
DR Pfam; PF01123; Staph_Strp_toxin; 1.
DR Pfam; PF02876; Staph_Strp_tox_C; 1.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; FALSE_NEG.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Toxin; Signal; Complete proteome.
FT SIGNAL 1 32 POTENTIAL.
FT CHAIN 33 236 EXOTOXIN TYPE H.
SQ SEQUENCE 236 AA; 27485 MW; 16352923907AD40D CRC64;
Query Match. 16.8%; Score 203; DB 1; Length 236;
Best Local Similarity 27.5%; Pred. No. 2.9e-09;
Matches 65; Conservative 43; Mismatches 78; Indels 50; Gaps 12;
QY 34 RNISTIV----YEYSDIV-----IDFKTSNHL-----VTKLDVRDARDFFENSEM 76
Db :||| ||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 77 DEYAANDFTGDKIAVSPVPDNLYSK-----GKVRAY-----TYGGIT 116
Db :| :| :||| :||| :||| :||| :||| :||| :||| :|||
QY 117 PYOKTSPKIPNYNLINGKQISVPYNESITNKTTTVAQEIDLKVKFLIAQHQLRSS-G 175
Db :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 124 LTNSEKEIKVPNVNDKSG---OPPMFIFVNPKPVTAQEVDIKVRKLIIKKYDIYNRE 181

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CC EMBL; U40453; AAC48868.1; .
CC DR EMBL; X03929; CA27568.1; .
CC DR EMBL; AE009982; AAL97141.1; .
CC DR PIR; A26152; A26152.
CC DR PIR; S29659; S29659.
CC DR PDB; 1B12; 24-NOV-99.
CC DR InterPro; IPR001961; Staph/Strep_toxin.
CC DR Pfam; PF01123; Staph_Strp_toxin; 1.
CC DR Pfam; PF02876; Staph_Strp_toxin; 1.
CC DR PRINTS; PR00279; BACTRTOXIN.
CC DR PROSITE; PS00277; Staph_Strp_toxin_1; 1.
CC DR PROSITE; PS00278; Staph_Strp_toxin_2; 1.
KW Toxin; Signal; 3D-structure.
FT SIGNAL 1 30
FT CHAIN 31 251
FT DISULFID 117 128
FT CONFLICT 6 6
FT CONFLICT 17 18
FT CONFLICT 25 35
FT CONFLICT 40 40
FT CONFLICT 43 43
FT CONFLICT 47 59
FT CONFLICT 129 129
FT CONFLICT 165 178
FT SEQUENCE 251 AA; 29246 MW; 54001FE4CCCCBFC3 CRC64;

Query Match 16.2%; Score 195.5; DB 1; Length 251;
Best Local Similarity 23.8%; Pred. No. 1.2e-08;
Matches 73; Conservative 48; Mismatches 79; Indels 45; Gaps 16;

QY 5 KLIFSFTSIPFAL-ISRPFVFG-----LEVNNLLRNIIYST-IVYEVSDIV-----ID 50
Db 10 KMFVFLVTLFGLTISQVFAQDPDPSPQLHRSLVNLQNIYFLYEGDPVTHENVKSV 69
QY 51 FKTSHNLVTK-----KLDVRDARDFEINSEDEVAANDFTGDK-IAVESVP-FDW 99
Db 70 QLLSHDLIYNVSGPNYDKLTKELK-----NQEM-----ATLFK--DKNVDIYGVYYHL 116
QY 100 NYL-SKGKVTAIYTGITPYO--KTSIPKNIPVNLWINGKQISVPYNEISTNKTITVAQE 156
Db 117 CYLCENAEBSACIYGGVTHNHNLEIPKIKVWVSIDIGQ-SLSF-DIETNKKWTAQE 174
QY 157 IDLVRKFLIAQHLYSSG-SSYKSGRLVFTNDSNKSYPDLFYVGYRDKESIFKVKYKD 215
Db 175 LDYKVRKYLTDNKLQYTNLSPKSYETGIKF-IPKNKESFWDFPEPEFTQSKYLMYKD 233
QY 216 NKSFN 220
Db 234 NETLD 238

RESULT 8
ETXB STAAU
ID ETXB STAAU STANDARD; PRT; 266 AA.
AC P01552;
DT 21-JUL-1986 (Rel. 01, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Enterotoxin type B precursor (SEB).
GN ENTB.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8618029; PubMed=3957869;
RA Jones C.L., Khan S.A.;
RT "Nucleotide sequence of the enterotoxin B gene from Staphylococcus

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RT aureus.";
RL J. Bacteriol. 166:29-33(1986).
RN [2]
RP SEQUENCE OF 40-91 FROM N.A.
RX MEDLINE=85298255; PubMed=3898073;
RA Ranelli D.M., Jones C.L., Johns M.B., Mussey G.J., Khan S.A.;
RT "Molecular cloning of staphylococcal enterotoxin B gene in
RT Escherichia coli and Staphylococcus aureus.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:5850-5854(1985).
RN [3]
RP SEQUENCE OF 28-266 (S-6).
RX MEDLINE=71007902; PubMed=5470821;
RA Huang I.-Y., Bergdoll M.S.;
RT "The primary structure of staphylococcal enterotoxin B. 3. The
RT cyanogen bromide peptides of reduced and aminoethylated enterotoxin
RT B, and the complete amino acid sequence.";
RL J. Biol. Chem. 245:3518-3525(1970).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RX MEDLINE=93063291; PubMed=1436058;
RA Swaminathan S., Furey W.F. Jr., Fletcher J., Sax M.;
RT "Crystal structure of staphylococcal enterotoxin B, a superantigen.";
RL Nature 359:801-806(1992).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF COMPLEX WITH MHC II.
RX MEDLINE=94203282; PubMed=8152483;
RA Jardenzky T.S., Brown J.H., Gorga J.C., Stern L.J., Urban R.G.,
RA Chi Y.I., Stauffer C., Strominger J.L., Wiley D.C.;
RT "Three-dimensional structure of a human class II histocompatibility
RT molecule complexed with superantigen.";
RL Nature 368:711-718(1994).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF COMPLEX WITH TCR.
RX MEDLINE=95096298; PubMed=9881971;
RA Li H., Llera A., Tsuchiya D., Leder L., Ysern X., Schlievert P.M.,
RA Karjalainen K., Mariuzza R.A.;
RT "Three-dimensional structure of the complex between a T cell receptor
RT beta chain and the superantigen staphylococcal enterotoxin B.";
RL Immunity 9:807-816(1998).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
RX MEDLINE=98181012; PubMed=9514739;
RA Papageorgiou A.C., Tranter H.S., Acharya K.R.;
RT "Crystal structure of microbial superantigen staphylococcal
RT enterotoxin B at 1.5-A resolution: Implications for superantigen
RT recognition by MHC class II molecules and T-cell receptors.";
RL J. Mol. Biol. 277:61-79(1998).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
CC FAMILY.
CC
CC -----
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EMBL; M1118; AAA88550.1; .
PIR; A01815; ENSAB6.
PIR; S27360; S27360.
DR PDB; 1SEB; 20-JUN-96.
DR PDB; 2SEB; 28-JAN-98.
DR PDB; 3SEB; 27-MAY-98.
DR PDB; 1SE3; 16-JUN-97.
DR PDB; 1SE4; 15-OCT-97.
DR PDB; 1SBB; 04-MAR-99.
DR InterPro; IPR001961; Staph/Strep_toxin.
DR Pfam; PF01123; Staph_Strp_toxin; 1.
DR Pfam; PF02876; Staph_Strp_toxin; 1.

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DR PRINTS: PR00279; BACTRITOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Enterotoxin; Toxin; Signal; Superantigen; 3D-structure.
FT SIGNAL 1 27
FT CHAIN 28 266
FT DISULFID 120 140
FT CONFLICT 56 58
FT CONFLICT 69 77
FT CONFLICT 118 118
FT CONFLICT 128 130
FT CONFLICT 133 135
FT CONFLICT 149 150
FT CONFLICT 156 156
FT CONFLICT 185 186
FT CONFLICT 233 233
FT CONFLICT 246 247
SQ SEQUENCE 266 AA; 31436 MW; B6D417F61CF018B0 CRC64;

Query Match 13.5%; Score 162.5; DB 1; Length 266;
Best Local Similarity 25.4%; Pred. No. 5.3e-06;
Matches 57; Conservative 40; Mismatches 86; Indels 41; Gaps 9;

QY 28 DNNLLRNIVSTIVYEYSDIVDFKT---SHNLVTKKLDVRDARDFINSEMEYAAAND 83
Db 57 DNHVSALNVKSIQDFLDLIYSIKDKLGNIDNVRVEFKNKLDADKYKDYVDFGANY 116
QY 84 F-----KTGDKIAVFSVPFDNLYSKGVTAATYGGITPYKTSIPK--NIPVNLWIN 134
Db 117 YQCYFSEKKN-----DINSHGTDKRTKCTMGVTEHNGNQLDKYSIRVFEED 166
QY 135 GKQISVPYNEISNKTVTVAQEDIDKVRKFLIAHQHLYS-SGSSYKSGRLVFTNDNSDK 193
Db 167 GKNLL--SFDVQTKKRVTAQEDLDYLRHVLKKNKLYEFNNSPYETGYIKFIENSEFW 224
QY 194 YSF-----DLFYVGYRDKESIFKVKYKDKNSFNIDKIGHLDIEID 232
Db 225 YDMPAPGDKF-----DQSKYLMYINDNK-----MVDSDKDVKE 258

RESULT 9
ETXG_STAAH
ID ETXG_STAAH STANDARD; PRT; 258 AA.
AC O85382;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Enterotoxin type G precursor (SEG).
GN ENTG OR SEG OR SAV1824 OR SA1642.
OS Staphylococcus aureus (strain Mu50 / ATCC 700699),
OS Staphylococcus aureus (strain N315), and
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878, 158879, 1280;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN-FR1572;
RX MEDLINE=98298056; PubMed=9632603;
RA Munson S.H., Tremaine M.T., Betley M.J., Welch R.A.;
RT "Identification and characterization of staphylococcal enterotoxin
RT types G and I from Staphylococcus aureus.";
RL Infect. Immun. 66:3337-3348(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-Mu50 / ATCC 700699, and N315;
RX MEDLINE=21311952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;

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RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC -1- STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
CC FAMILY.
CC -----
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CC -----
DR EMBL; AF064773; AAC26660.1; -
DR EMBL; AP003363; BAB57986.1; -
DR EMBL; AP003135; BAB42910.1; -
DR HSP; P01552; ISBB.
DR InterPro; IPR001961; Staph_Strep_toxin.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_toxin; 1.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; FALSE_NEG.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Enterotoxin; Toxin; Signal; Superantigen; Complete proteome.
FT SIGNAL 1 25
FT CHAIN 26 258 ENTEROTOXIN TYPE G.
FT DISULFID 116 133 BY SIMILARITY.
SQ SEQUENCE 258 AA; 29940 MW; E298210170D012C CRC64;

Query Match 13.3%; Score 161; DB 1; Length 258;
Best Local Similarity 28.9%; Pred. No. 6.7e-06;
Matches 63; Conservative 43; Mismatches 62; Indels 50; Gaps 15;

QY 19 SRPVGLEVDNNSLLRNIVSTIVYEYSDIV--IDFKTSHNLVTKKLDVRDARDFINSEM 76
Db 56 SPVVEG-----RGVINSRQFLSHDLTFPIEYK-SYNEVKTELE-----NTEL 96
QY 77 DEYAANDFKTGDKIAVFSVPFDNLYL---SKGKVT-----AYYGGIT-PYKTSIPKNI 127
Db 97 -----ANNYK-DKKVDIFGVFYFTCIIPKSEPDINQNGGCMYGLTFNSENEDKLI 151
QY 128 PVNLWINGKQISVPYNEISNKTVTVAQEDIDKVRKFLIAHQHLYS-SGSSYKSGRLVFEH 186
Db 152 TVQVTIDNRQ-SLGFT-ITTKNNWVTIQELDVKARHHLTKKKLYEPDGFSAFESGYIKF- 208
QY 187 TNDNSDKYSFDLF-----YGYRDKESIFKVKYKDKN 217
Db 209 TEKNTSFWFDLPKPKELVPFVPYK----FLNIYGDNK 242

RESULT 10
ETC2_STAAU
ID ETC2_STAAU STANDARD; PRT; 266 AA.
AC P34071;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Enterotoxin type C-2 precursor (SEC2).
GN ENTC2.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-66.
RX MEDLINE=89277549; PubMed=2543637;
RA Bohach G.A., Schlievert P.M.;
RT "Conservation of the biologically active portions of staphylococcal
RT enterotoxins C1 and C2.";
RL Infect. Immun. 57:2249-2252(1989).
RN [2]

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FT CHAIN 28 266 ENTEROTOXIN TYPE C-3.
FT DSULFID 120 137
SQ SEQUENCE 266 AA; 5ED8A32D11FFCA59 CRC64;

Query Match 12.9%; Score 156; DB 1; Length 266;
Best Local Similarity 26.18; Pred. No. 1.7e-05;
Matches 54; Conservative 42; Mismatches 63; Indels 48; Gaps 10;

Qy 40 IYVEYSDIVDFKTSNHLVTKLVDARDARDFINSEMDYAA-----DFKTGDKIAVFS 94
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 76 LIYNISDKKL---KNYDKVKTELLNEDLAKKYKDEVDVYGSNYVNCYFSSKDNV----- 128

Qy 95 VPFDNVLYSKQV-----AYTGGTTPQKTSIP-----KNIPVNLWINGKQISVPYNEIST 147
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 129 -----CKVTGGKTCMYGGITKHEGHNFDNGNLVLRVYEN-KRNTISF-EVQT 176
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

Qy 148 NKTTVTAQEIOLKYRKFLIAHQHLYSSGSS-YKSGRLVFHNDNS-----DKYS 195
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 177 DKSVTAQELDIKARNFELINKNLYEFNSSPYETGYIKFIENNNGTFWYDMMPAGDKFD 236

Qy 196 FDLFVGVYRKESIFKYVKNKSFNID 222
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 237 QSKYLMYNDNKT-----DSKSVKIE 258

RESULT 12
ETCI_STAAU STANDARD; PRT; 266 AA.
AC PO1553;
Dt 21-JUL-1986 (Rel. 13, Created)
Dt 01-JAN-1990 (Rel. 13, Last sequence update)
Dt 15-JUN-2002 (Rel. 41, Last annotation update)
DE Enterotoxin type C-1 precursor (SECI).
GN ETCI.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88038352; PubMed=2823067;
RA Bohach G.A., Schlievert P.M.;
RT "Nucleotide sequence of the staphylococcal enterotoxin C1 gene and
RL relatedness to other pyrogenic toxins.";
RN Mol. Gen. Genet. 209:15-20(1987).
RN [2]
RP SEQUENCE OF 28-266.
RX MEDLINE=8321337; PubMed=6189824;
RA Schmidt J.J., Spero L.;
RT "The complete amino acid sequence of staphylococcal enterotoxin C1.";
RN J. Biol. Chem. 258:6300-6306(1983).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
CC FAMILY.
CC -----
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CC -----
CC EMBL; X05815; CAA29260.1; --
CC PIR; A01816; ENSACL.
CC PIR; S06356; S06356.
CC HSP; P34071; LSE2.
CC InterPro; IPR001961; Staph_Strep_toxin.
CC Pfam; PF01123; Staph_Strep_toxin; 1.
CC Pfam; PF02876; Staph_Strep_toxin_C; 1.
CC PRINTS; PR00279; BACTRLTXIN.
CC PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.

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RP X-RAY CRYSTALLOGRAPHY (2.05 ANGSTROMS).
RX MEDLINE-97337442; PubMed-9194182;
RA Prasad G.S., Radhakrishnan R., Mitchell D.T., Earhart C.A.,
RA Dinges M.M., Cook W.J., Schlivert P.M., Ohlendorf D.H.,
RT "Refined structures of three crystal forms of toxic shock syndrome toxin-1 and of a tetramutant with reduced activity.";
RL Protein Sci. 6:1220-1227(1997).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS) OF MUTANTS.
RX MEDLINE-98254504; PubMed-9585531;
RA Earhart C.A., Mitchell D.T., Murray D.L., Pinheiro D.M., Matsumura M.,
RA Schlivert P.M., Ohlendorf D.H.,
RT "Structures of five mutants of toxic shock syndrome toxin-1 with reduced biological activity.";
RL Biochemistry 37:7194-7202(1998).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DISEASE: THIS TOXIN IS RESPONSIBLE FOR THE SYMPTOMS OF TOXIC SHOCK SYNDROME.
CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN FAMILY.
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DR EMBL; J02615; AAA26682.1; -
DR PIR; A24606; XCSASI.
DR PDB; 2TS5; 24-DEC-97.
DR PDB; 3TSS; 24-DEC-97.
DR PDB; 4TSS; 24-DEC-97.
DR PDB; 5TSS; 24-DEC-97.
DR PDB; 1Q1L; 12-AUG-97.
DR PDB; 2Q1L; 12-AUG-97.
DR PDB; 1AW7; 18-NOV-98.
DR PDB; 1TS2; 16-DEC-98.
DR PDB; 1TS3; 16-DEC-98.
DR PDB; 1TS4; 16-DEC-98.
DR PDB; 1TS5; 16-DEC-98.
DR InterPro; IPR001961; Staph/Strep_toxin.
DR InterPro; IPR003999; Staph_toxin.
DR Pfam; PF01123; Staph_strip_toxin; 1.
DR Pfam; PF02876; Staph_strip_tox_C; 1.
DR PRINTS; PR01501; TOXICSSSTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; FALSE_NEG.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR Toxin; Superantigen; Signal; 3D-structure.
DR SIGNAL 1 40
FT CHAIN 41 234 TOXIC SHOCK SYNDROME TOXIN-1.
SQ SEQUENCE 234 AA; 26306 MW; E95789FF9A1D7AB4 CRC64;
Query Match 9.3%; Score 112.5; DB 1; Length 234;
Best Local Similarity 21.1%; Pred. No. 0.041;
Matches 53; Conservative 35; Mismatches 98; Indels 65; Gaps 9;
QY 29 NNSLLRNIYTIYVEYSDIVDFK-----TSHNLV-TKKLDVRD-----ARDFFI 72
DB 2 NKLLMNFVTSPLLLATTATDFTVPVLSNQIIRKAKASTNDNIKDLLDWYSSGSDTET 61
QY 73 NSEV-----DEVAANDKTDGKIAVSPFDDN-----Y 101
DB 62 NSEVLNLSGMRIRKIKTDGSGISLIIPSPYSPAFKGEKV-----DUNTRTKKSOH 114
QY 102 LSKGKVATYTGITPYQKTSIPKNIPLNWLINGKQISVPIYNEISTNKTIVTAQAEIDLKV 161
DB 115 TSEGTYIHQISGVNTKLPTELPLKVKVHGKDSPLKYGK-PKDKQLAISTLDLFEI 173
QY 162 RKFLIAHQIYSSGSSKSRVFNHNDNSDKYSFDLFYVGYRDKESIFKVKYDNKNSFNI 221
DB 174 RHQLTOIHGLYR--SSDKTGGYWKITMNDGSTYQSOL-----SKKFEYNTKPPINI 223

QY 222 DKIGHLDIED 232
DB 224 DEIKTIEAEIN 234
RESULT 14
YKKL_CAEEL
ID YKKL_CAEEL STANDARD; PRT; 1010 AA.
AC P34278;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein C02F5.1 in chromosome III.
GN C02F5.1
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Briscot N2;
RX MEDLINE-94150718; PubMed-7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favell A., Fraser A.,
RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
RA Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,
RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Shawhagen R.,
RA Sims M., Smalton N., Smith A., Smith M., Sonhammer E., Staden R.,
RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
RA Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
RA Wohldman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans.";
RL Nature 368:32-38(1994).
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DR EMBL; L14745; AAA27916.2; -
DR WormPep; C02F5.1; CE02450.
KW Hypothetical protein.
SQ SEQUENCE 1010 AA; 113231 MW; 15E19DD975824D94 CRC64;
Query Match 8.8%; Score 106.5; DB 1; Length 1010;
Best Local Similarity 22.0%; Pred. No. 0.73;
Matches 51; Conservative 48; Mismatches 90; Indels 43; Gaps 10;
QY 3 KTKLIFSFTSIFTAISRPFVGLVDDNLSLRNIYTIYVEYSDIVDFKTSNHLVTKKL 62
DB 213 ETNHNVTNLEAAEMDT-----KLDENNTMNAIRIPINSNVPVMDITEHHTLIBEK- 267
QY 63 DVRDARDFFINSMDVYAANDFTGDKIAVSPFDDNLSKGVATYTGITPYQKTS 122
DB 268 ----KNDTGPQLMDISAPQVQVNDTALFNSPRD--ICNKL-----GV-PQLIN 313
QY 123 IPKN-TPVNLWINGKQISVPIYNEISTNKTIVTAQAEIDLKVKRFLIAHQIYSSGSSYKSG 181
DB 314 IASNVYVDMIDITQAV---LNAEKNDQFETSQLMDISIPKVLV-----NDT 358
QY 182 RLVEHTNDNSDKYSFDLFYVGYRDKESIFKVKYDNKNSFNI-DKIGHLDIED 232
DB 359 MAMFNPKHVSSMDL-----EKTIEAANDKSTKYPSTADEVEDLDMDMD 403
RESULT 15

YPX5_CAEEL
ID YPX5_CAEEL STANDARD; PRT; 1216 AA.
AC Q09277;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Hypothetical 133.3 kDa protein F40H6.5 in Chromosome III.
GN F40H6.5.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Du Z.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: STRONG, TO C.ELEGANS F40H6.2.
CC -----
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CC -----
DR EMBL; U21310; AAA62522.1; -;
DR WormPep; F40H6.5; CE01937;
DR InterPro; IPR004024; DUF225.
DR InterPro; IPR001079; Galectin.
DR Pfam; PF02795; DUF225; 1.
DR SMART; SM00276; GLECT; 1.
KW Hypothetical protein; Transmembrane.
FT TRANSMEM 3 23 POTENTIAL.
FT TRANSMEM 181 201 POTENTIAL.
FT TRANSMEM 377 397 POTENTIAL.
FT TRANSMEM 440 460 POTENTIAL.
FT TRANSMEM 781 801 POTENTIAL.
FT TRANSMEM 1174 1194 POTENTIAL.
SQ SEQUENCE 1216 AA; 13313 MW; B5C30EBDA014D793 CRC64;

Query Match 8.58; Score 103; DB 1; Length 1216;
Best Local Similarity 22.38; Pred. No. 1.7;
Matches 44; Conservative 30; Mismatches 69; Indels 54; Gaps 9;

QY 8 FSFTSI--FIAIISRPVGL--EVDNNSL-----LRNIYSTIVY-----EYSDIVID-F 51
Db 478 FYFVSLYTFGRSVTSKVIAGIAFETEENSCGLNLPVIRELYKDRYVYVAGNDYQYLDDGY 537
QY 52 KTSNLYTKKLDVRDARDFEINSEMDVA-----ANDFKTGDKIAVFSVPFDWN 100
Db 538 NITGNIVGYVDCKDSKDEFYVGHLPVSFAFTTSSMTTASDSTSDSVI----- 589
QY 101 YLSKGKVTAYTYGGITPYQKTSIPKPNVNLWNGKQISVPYNEISTNKTWTTAQEIDLK 160
Db 590 -VSSSKNPVSNPFTTYSLPSSPNN-----PFISITTPDSASSQ-----K 630
QY 161 VRKFLIAHQHLYSSGSS 177
Db 631 ISTTTAISHSAYSASPS 647

Search completed: February 14, 2003, 13:44:25
Job time : 14 secs

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OM protein - protein search, using sw model

Run on: February 14, 2003, 13:44:09 ; Search time 13 Seconds

(without alignments)
457.914 Million cell updates/sec

Title: US-09-869-136-2

Perfect score: 1207

Sequence: 1 MKKTKLIFSFTSIFIAISR.....KDNKSFNIDKIGHLDIEIDS 233

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 140259 seqs, 25548876 residues

Total number of hits satisfying chosen parameters: 140259

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA.*

1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pdb.pdb.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pdb.pdb.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pdb.pdb.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pdb.pdb.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pdb.pdb.*
6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pdb.pdb.*
7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pdb.pdb.*
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11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pdb.pdb.*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pdb.pdb.*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pdb.pdb.*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pdb.pdb.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|---------------------|-------------------|
| 1 | 255.5 | 21.2 | 257 | US-09-870-759-8 | Sequence 8, Appl |
| 2 | 251 | 20.8 | 248 | US-09-870-759-16 | Sequence 16, Appl |
| 3 | 251 | 20.8 | 258 | US-09-870-759-14 | Sequence 14, Appl |
| 4 | 239.5 | 19.2 | 231 | US-08-882-431-2 | Sequence 2, Appl |
| 5 | 231.5 | 19.2 | 233 | US-08-882-431-4 | Sequence 4, Appl |
| 6 | 195.5 | 16.2 | 251 | US-08-882-431-16 | Sequence 16, Appl |
| 7 | 195.5 | 16.2 | 251 | US-08-882-431-13 | Sequence 13, Appl |
| 8 | 167.5 | 13.9 | 239 | US-08-882-431-10 | Sequence 10, Appl |
| 9 | 162.5 | 13.5 | 239 | US-09-150-947B-12 | Sequence 12, Appl |
| 10 | 162.5 | 13.5 | 266 | US-09-870-759-18 | Sequence 10, Appl |
| 11 | 153.5 | 12.7 | 266 | US-08-882-431-14 | Sequence 14, Appl |
| 12 | 153.5 | 12.7 | 266 | US-09-870-759-12 | Sequence 12, Appl |
| 13 | 132.5 | 12.6 | 265 | US-08-882-431-8 | Sequence 8, Appl |
| 14 | 148.5 | 12.3 | 265 | US-08-882-431-6 | Sequence 6, Appl |
| 15 | 122 | 10.1 | 250 | US-09-870-759-20 | Sequence 20, Appl |
| 16 | 112.5 | 9.3 | 234 | US-09-870-759-18 | Sequence 18, Appl |
| 17 | 111 | 9.2 | 233 | US-08-882-431-12 | Sequence 12, Appl |
| 18 | 96.5 | 8.0 | 226 | US-09-815-242-5900 | Sequence 5900, Ap |
| 19 | 96.5 | 8.0 | 226 | US-09-815-242-13156 | Sequence 13156, A |

20 87.5 7.2 451 9 US-09-910-186A-12 Sequence 12, Appl
21 84.5 7.0 445 10 US-09-815-242-5010 Sequence 5010, Ap
22 84.5 7.0 447 10 US-09-815-242-10908 Sequence 10908, A
23 84.5 7.0 951 9 US-09-824-097-15 Sequence 15, Appl
24 83.5 6.9 362 9 US-09-839-894-31 Sequence 31, Appl
25 82.5 6.8 788 9 US-09-738-626-6722 Sequence 6722, Ap
26 82.5 6.8 788 9 US-09-908-193-35 Sequence 35, Appl
27 82.5 6.8 818 9 US-10-055-364-44 Sequence 44, Appl
28 82 6.8 664 12 US-10-067-385-6 Sequence 6, Appl
29 82 6.8 1007 10 US-09-765-272-216 Sequence 216, App
30 82 6.8 1049 9 US-09-978-295A-496 Sequence 496, App
31 82 6.8 1049 9 US-09-978-697-496 Sequence 496, App
32 82 6.8 1049 9 US-09-978-192A-496 Sequence 496, App
33 82 6.8 1049 9 US-09-999-832A-496 Sequence 496, App
34 82 6.8 1049 9 US-09-978-189-496 Sequence 496, App
35 82 6.8 1049 9 US-10-028-072-358 Sequence 358, App
36 82 6.8 1049 9 US-10-121-049-358 Sequence 358, App
37 82 6.8 1049 9 US-10-123-904-358 Sequence 358, App
38 82 6.8 1049 9 US-10-140-470-358 Sequence 358, App
39 82 6.8 1049 9 US-10-095-627-1 Sequence 1, Appl
40 82 6.8 1049 9 US-10-175-746-358 Sequence 358, App
41 82 6.8 1049 9 US-10-176-918-358 Sequence 358, App
42 82 6.8 1049 9 US-10-176-921-358 Sequence 358, App
43 81.5 6.8 463 9 US-09-816-467-2 Sequence 2, Appl
44 81 6.7 359 9 US-09-839-894-29 Sequence 29, Appl
45 79 6.5 619 10 US-09-801-368-88 Sequence 88, Appl

ALIGNMENTS

RESULT 1
US-09-870-759-8
; Sequence 8, Application US/09870759
; Patent No. US2002017755A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASES.
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-870-759-8

Query Match 21.2%; Score 255.5; DB 9; Length 257;
Best Local Similarity 29.9%; Pred. No. 1.8e-16;
Matches 58; Conservative 41; Mismatches 58; Indels 37; Gaps 7;

QY 44 YSDIVIDFKTSHNLVTKKLDVRDARDFINSEMDVAANDFKTGKIAVFSVPDKNYLS 103
Db 88 YNDLLVDF-----DSKDIVDKYKGVLDYAY-----IGYOC 120
QY 104 KG---KVTATYTGITPYQKTSI--PKNIPVNLWINGKOISYPYNEISTNKTVTVAQEID 158
Db 121 AGGTPNKTAACMGVGTLDHNNRLTEKKVPINLWLDGKQNTVPLETVTKNKNVQVLELD 180
QY 159 LKVRFLTAQHOLYSS---GSSYKSGRLVFTHTNDNSDKYSFOLFVYGVYRDKSIFKVKYD 215
Db 181 LQARYLQAEKYNLYNSDVPDGVQVGLIVFHTS--TEPSYNYDLFGAQGQNSNTLLRIYRD 239
QY 216 NKSENIIDKIGHDI 229
Db 240 NKTINSENH-HIDI 252

RESULT 2

Qy 159 LKVRKFLIAQHLYSS---GSSYKSGRLVFTHTNDNSDKYSFDLFYVGYRDKESIFKVKYKD 215
Db 181 LQARYLQEKYLNLYNSVDGKVRQGLIVFHTS--TEPSVNYDLFGAQGOYSNTLLRIYED 239
Qy 216 NKSEFNIDKIGHLDI 229
Db 240 NKTINSENN-HIDI 252

RESULT 5
US-08-882-431-4
; Sequence 4, Application US/08882431
; Publication No. US20030009015A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John Moran
; STREET: US Army MRC -504 Scott Street MCMR-JA (John Moran-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Moran, John
; REGISTRATION NUMBER: 26,313
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
US-08-882-431-4

Query Match 19.2%; Score 231.5; DB 1; Length 233;
Best Local Similarity 28.9%; Pred. No. 2.7e-14;
Matches 56; Conservative 38; Mismatches 63; Indels 37; Gaps 7;

Qy 44 YSDIVDFKTSNLTVKKLDVRDARDFINSEMDYAAANDFKTGDKIAVFSVPEDWNYLS 103
Db 64 YNDLVRF-----DSKDIVDYKGGKVDLYGAYA-----GYQC 96

Qy 104 KG---KVTATYGGITPYQKTSI---PKNPVNLWNGKQISVPYNEISNTKTTVTAQED 158
Db 97 AGGTPNKTACMYGGVTLHDNRLTEERKVPINLWLDGKQNTVPLETKVTKNKNVTQDLD 156

Qy 159 LKVRKFLIAQHLYSS---GSSYKSGRLVFTHTNDNSDKYSFDLFYVGYRDKESIFKVKYKD 215
Db 157 KQARYLQEKYLNLYNSVDGKVRQGLIVFHTS--TEPSVNYDLFGAQGOYSNTLLRIYED 215
Qy 216 NKSEFNIDKIGHLDI 229

Db 216 NKTINSENN-HIDI 228

RESULT 6
US-08-882-431-16
; Sequence 16, Application US/08882431
; Publication No. US20030009015A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John Moran
; STREET: US Army MRC -504 Scott Street MCMR-JA (John Moran-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Moran, John
; REGISTRATION NUMBER: 26,313
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
US-08-882-431-16

Query Match 16.2%; Score 195.5; DB 1; Length 251;
Best Local Similarity 29.8%; Pred. No. 6.5e-11;
Matches 73; Conservative 48; Mismatches 79; Indels 45; Gaps 16;

Qy 5 KLIFSFTSIFTAI-ISRPFVG-----LEVNNLSLRNIYST-IVYEYSDIV-----ID 50
Db 10 KMVFVLTFTGLTISQEVFAQQDDPSQLHRSSULKQNIYFLYEGDPYTHENKVSVD 69
Qy 51 FKTSHNLVTK-----KLDVRDARDFINSEMDYAAANDFKTGDK-IAVFSVP-FDW 99
Db 70 QLRSHDLIYVSGPNYDKLTKTELK-----NQEN-----ATLEK--DKNVDIYGYEYVHL 116

Qy 100 NYL-SKGKVTATYGGITPYO--KTSIPKNIPVNLWNGKQISVPYNEISNTKTTVTAQ 156
Db 117 CYLCENAEARSACIYGGVTNHGEGNHLEIPKIKVVKVSDIGIQ-SLSF-DIETNKKMVT 174

Qy 157 IDLVKRFELIAQHLYSSG--SSYKSGRLVFTHTNDNSDKYSFDLFYVGYRDKESIFKVKYKD 215
Db 175 LDYKVRKFLTDKNOLYNGPSKYETGIKF-IPKNKESFDFPFPEFTQSKYLMYKD 233

Qy 216 NKSEFN 220
Db 234 NETLD 238

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: Apple Maci

QY 28 DNSSLRNITVYEVSDIVDFKT-----SHNLVTKLDVRDARDFFINSEMDYEAAND 83
 Db 30 DNHVSAINVKSIDQFLYDIYSIKDTKLGNDYDNRVFEKNDLADKYDKYVDFEGANY 89
 QY 84 F-----KTGDKIAVSPEDWNLKSGKVTAYTYGGITPYQKTSIPK--NIPVNLWIN 134
 Db 90 YQCYFESKTN-----DINSHOTDKRKTCTMYGGVTEHNGNQLDKYRSITVRVFE 139
 QY 135 GKQISVPYNEISTNKTVTVAEIDLKVRKFLIAQHOLYS--SGSSYSKGRVLVPHFTNDNSDK 193
 Db 140 GKNLL--SFDVQTNKKKVTAEQDLVLRHYLVKNNKLYEFNNSPYETGYIKFIENENSW 197
 QY 194 YSF-----DLFVGVGRDRESIFKVKDKNSFNIDKIGHLDIEID 232
 Db 198 YDMPAPGDKF-----DQSKYLMYNDNK-----MYDSKDVKIE 231

RESULT 10

US-09-870-759-10
 ; Sequence 10, Application US/09870759
 ; Patent No. US20020177551A1
 ; GENERAL INFORMATION:
 ; APPLICANT: TERMAN, David S
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
 ; FILE REFERENCE: 870759
 ; CURRENT APPLICATION NUMBER: US/09/870,759
 ; CURRENT FILING DATE: 2002-01-14
 ; PRIOR APPLICATION NUMBER: US 60/208,128
 ; PRIOR FILING DATE: 2000-05-30
 ; NUMBER OF SEQ ID NOS: 166
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 10
 ; LENGTH: 266
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus aureus
 US-09-870-759-10

Query Match 13.5%; Score 162.5; DB 9; Length 266;
 Best Local Similarity 25.4%; Pred. No. 8e-08;
 Matches 57; Conservative 40; Mismatches 86; Indels 41; Gaps 9;

QY 28 DNSSLRNITVYEVSDIVDFKT-----SHNLVTKLDVRDARDFFINSEMDYEAAND 83
 Db 57 DNHVSAINVKSIDQFLYDIYSIKDTKLGNDYDNRVFEKNDLADKYDKYVDFEGANY 116
 QY 84 F-----KTGDKIAVSPEDWNLKSGKVTAYTYGGITPYQKTSIPK--NIPVNLWIN 134
 Db 117 YQCYFESKTN-----DINSHOTDKRKTCTMYGGVTEHNGNQLDKYRSITVRVFE 166
 QY 135 GKQISVPYNEISTNKTVTVAEIDLKVRKFLIAQHOLYS--SGSSYSKGRVLVPHFTNDNSDK 193
 Db 167 GKNLL--SFDVQTNKKKVTAEQDLVLRHYLVKNNKLYEFNNSPYETGYIKFIENENSW 224
 QY 194 YSF-----DLFVGVGRDRESIFKVKDKNSFNIDKIGHLDIEID 232
 Db 225 YDMPAPGDKF-----DQSKYLMYNDNK-----MYDSKDVKIE 258

RESULT 11

US-08-882-431-14
 ; Sequence 14, Application US/08882431
 ; Publication No. US20030009015A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Robert G. Ulrich,
 ; APPLICANT: Mark A. Olson
 ; APPLICANT: Sina Bavari
 ; TITLE OF INVENTION: Bacterial Superantigen
 ; NUMBER OF SEQUENCES: 16
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: John Moran
 ; STREET: US Army MRC -504 Scott Street MCMR-JA (John Moran-Patent Atty)

CITY: FORT DETRICK
 STATE: MARYLAND
 COUNTRY: USA
 ZIP: 21702-5012
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Apple Macintosh
 OPERATING SYSTEM: Macintosh 7.5
 SOFTWARE: Microsoft Word 6.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/882,431
 FILING DATE: June 25, 1997
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Moran, John
 REGISTRATION NUMBER: 26,313
 REFERENCE/DOCKET NUMBER:
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (301) 619-2065
 TELEFAX: (301) 619-7714
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 266
 TYPE: Amino Acid
 STRANDEDNESS: Unknown
 TOPOLOGY: Unknown
 MOLECULE TYPE: Peptide
 US-08-882-431-14

Query Match 12.7%; Score 153.5; DB 1; Length 266;
 Best Local Similarity 28.5%; Pred. No. 5.4e-07;
 Matches 55; Conservative 41; Mismatches 60; Indels 37; Gaps 12;
 QY 55 HNLVTKLDVRDARDFFINSE--MDEYANDFTGKIAVSPVFDWN--YLSK----GKVT 108
 Db 78 YNISDKLKNYDK-----VKTELLNGLAKYK--DEVVDYGSNYVYVNCYFSSKDNVGVKT 132
 QY 109 ---ATYGGITPYQKTSIP-----KNIPVNLWINGKQISVPYNEISTNKTVTVAEIDLKV 161
 Db 133 GKGTCMYGGITKHEGNHFNQNLVNLIRYEN--KRNTISF--EVOTDKKSVTAQELDIKA 190
 QY 162 RKFLTAQHLYSSGSS--YKSGRLVPHFTNDNS-----DKYSFDLFPYGVYRDKESI 209
 Db 191 RNFLINKNLNLYEFNSFVETGYIKFIENNGNTFYDMPAPGDKFDQSKYLMYNDNRKV 250
 QY 210 FKVYKDKNSFNID 222
 Db 251 -----DSKSVKIE 258

RESULT 12

US-09-870-759-12
 ; Sequence 12, Application US/09870759
 ; Patent No. US20020177551A1
 ; GENERAL INFORMATION:
 ; APPLICANT: TERMAN, David S
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
 ; FILE REFERENCE: 870759
 ; CURRENT APPLICATION NUMBER: US/09/870,759
 ; CURRENT FILING DATE: 2002-01-14
 ; PRIOR APPLICATION NUMBER: US 60/208,128
 ; PRIOR FILING DATE: 2000-05-30
 ; NUMBER OF SEQ ID NOS: 166
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 12
 ; LENGTH: 266
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus aureus
 US-09-870-759-12

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Db      57  DNHVSAINVA$IDQFYFDLIYSIKOTKLGIDYNRVFEKKNDLADKYDKYVDVFGAN- 115
QY      84  FKTDKIAVSVPP-----DWNVLSGKVTAYVYGGITPYOKTSIPK--NIPVNLWINK 136
Db     116  -----AYQCAFSKKTNDINSHQTDKRKTCMYGGVTEHNGQLDKYRSITVRVEDGK 168
QY     137  QI-----SVPYNEISTNKTVAQIDILUKVRFLAQHLYS-SSGSYKSGRLVFHTNDN-- 190
Db     169  NLLSFDVQY-----NKKKVTAQELDYLTRHLYLVKNKLYEFNNSPETGYIAFIENQNF 223
QY     191  -----SDKYSFDLFFVGYGRKESIFKVVYKDNK 217
Db     224  YDMNPAPGDRF-----DQSKVLMYNDNK 247

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RESULT 14
US-08-882-431-6
; Sequence 6, Application US/08882431
; Publication No. US2003009015A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John Moran
; STREET: US Army NMMC -504 Scott Street MCMR-JA (John Moran-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431
; FILING DATE: June 25, 1997

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1  REGISTRATION NUMBER: 26,313
2
3  REFERENCE/DOCKET NUMBER:
4
5  TELECOMMUNICATION INFORMATION:
6
7  TELEPHONE: (301) 619-2065
8
9  TELEFAX: (301) 619-7714
10
11 INFORMATION FOR SEQ ID NO: 6:
12
13 SEQUENCE CHARACTERISTICS:
14
15 LENGTH: 265
16
17 TYPE: Amino Acid
18
19 STRANDEDNESS: Unknown
20
21 TOPOLOGY: Unknown
22
23 MOLECULE TYPE: Peptide
24
25 US-08-882-431-6

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Db      76  LYSIRDTKLGDDYDNRVEKN-----KDLADKYDKYVDVGANYNYQCYESK 124
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QY      85  KTGDKTAVSPVDPNYLKSGKVATYTGGITPYQKTSIPK--NIPVLNWKNGKI---S 139
      ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
Db      125  KTN-----DINSHOTDKRKTCMYGGVTEHNGNQLDKYSITRVFVEDGKNLISFD 174

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Job time : 14 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 14, 2003, 13:44:04 ; Search time 36 Seconds

(without alignments)
862.428 Million cell updates/sec

Title: US-09-869-136-2

Perfect score: 1207

Sequence: 1 MKTKLIFSFTSIFALISR.....KDNKSFNIDKIGHLDIEIDS 233

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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- 2: /SID22/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
- 3: /SID22/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
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- 10: /SID22/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
- 11: /SID22/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
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- 23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-----------------------------|
| 1 | 1207 | 100.0 | 233 | 21 | AA193741 Amino acid sequenc |
| 2 | 1126 | 93.3 | 258 | 23 | ABP29565 Streptococcus poly |
| 3 | 305 | 25.3 | 235 | 23 | ABP29257 Streptococcus poly |
| 4 | 297 | 24.6 | 235 | 19 | AAW62787 Mutant streptococc |
| 5 | 297 | 24.6 | 235 | 19 | AAW62788 Mutant streptococc |
| 6 | 296 | 24.5 | 235 | 19 | AAW62784 Streptococcal pyro |
| 7 | 285.5 | 23.7 | 208 | 12 | AA13210 Streptococcal ent |
| 8 | 285.5 | 23.7 | 208 | 14 | AA13210 Streptococcal ent |
| 9 | 285.5 | 23.7 | 208 | 22 | AA13210 Streptococcus pyro |
| 10 | 285.5 | 23.7 | 208 | 23 | ABP76241 Staphylococcus pyo |

| | | | | | |
|----|-------|------|-----|----|-----------------------------|
| 11 | 274 | 22.7 | 235 | 19 | AAW62785 Mutant streptococc |
| 12 | 270 | 22.4 | 235 | 19 | AAW62786 Mutant streptococc |
| 13 | 259 | 21.5 | 232 | 23 | ABP29143 Streptococcus poly |
| 14 | 258.5 | 21.4 | 257 | 22 | AAU14103 Peptide sequence f |
| 15 | 256 | 21.2 | 230 | 22 | AAU67339 Staphylococcus aur |
| 16 | 256 | 21.2 | 245 | 18 | AAW35374 Staphylococcus ent |
| 17 | 252 | 20.9 | 245 | 18 | AAW35375 Staphylococcus ent |
| 18 | 251.5 | 20.8 | 233 | 18 | AAW35373 Staphylococcus ent |
| 19 | 251.5 | 20.8 | 233 | 18 | AAW06738 Staphylococcus ent |
| 20 | 251.5 | 20.8 | 257 | 22 | AAU14104 Peptide sequence f |
| 21 | 248.5 | 20.6 | 228 | 14 | AA13210 Streptococcal ent |
| 22 | 248.5 | 20.6 | 228 | 22 | AAW67340 Staphylococcus aur |
| 23 | 248.5 | 20.6 | 228 | 23 | ABP76236 Staphylococcus aur |
| 24 | 245.5 | 20.3 | 259 | 23 | ABP29357 Streptococcus poly |
| 25 | 244.5 | 20.3 | 233 | 14 | AA13205 Staphylococcal ent |
| 26 | 244.5 | 20.3 | 233 | 22 | AAW67338 Staphylococcus aur |
| 27 | 243 | 20.1 | 234 | 21 | AA13205 Streptococcus poly |
| 28 | 241.5 | 20.0 | 233 | 23 | ABP29092 Streptococcus aur |
| 29 | 241.5 | 20.0 | 233 | 23 | ABP76234 Staphylococcus aur |
| 30 | 240.5 | 19.9 | 228 | 12 | AA13205 Staphylococcal ent |
| 31 | 239.5 | 19.8 | 233 | 21 | AA13205 Amino acid sequenc |
| 32 | 239.5 | 19.8 | 233 | 23 | ABP29502 Staphylococcal ent |
| 33 | 239.5 | 19.8 | 257 | 21 | AA13205 Staphylococcal ent |
| 34 | 239.5 | 19.8 | 257 | 23 | ABP79501 Staphylococcal ent |
| 35 | 234.5 | 19.4 | 233 | 12 | AA13203 Staphylococcal ent |
| 36 | 231.5 | 19.2 | 233 | 21 | AA13203 Mutant Staphylococ |
| 37 | 228 | 18.9 | 230 | 12 | AA13204 Staphylococcal ent |
| 38 | 228 | 18.9 | 230 | 14 | AA13204 Staphylococcal ent |
| 39 | 225 | 18.6 | 230 | 23 | ABP76235 Staphylococcus aur |
| 40 | 203 | 16.8 | 236 | 21 | ABP29358 Amino acid sequenc |
| 41 | 203 | 16.8 | 236 | 23 | ABP29358 Streptococcus poly |
| 42 | 200.5 | 16.6 | 251 | 18 | AAW12153 Streptococcus pyog |
| 43 | 200 | 16.6 | 250 | 18 | AAW12145 Streptococcus pyog |
| 44 | 199.5 | 16.5 | 251 | 18 | AAW12151 Streptococcus pyog |
| 45 | 196.5 | 16.3 | 251 | 18 | AAW12146 Streptococcus pyog |

ALIGNMENTS

RESULT 1
AA193741
ID AA193741 standard; Protein; 233 AA.
XX
AC AA193741;
XX
XX 03-OCT-2000 (first entry)
XX
XX Amino acid sequence of the mature SMEZ-2 superantigen protein.
XX
XX Sperantigen; SMEZ-2; SPE-G; SPE-H; SPE-J; Streptococcal disease;
XX
XX Kawasaki syndrome; T cell activation; cancer therapy.
XX
XX Streptococcus pyogenes.
XX
XX WO200039159-A1.
XX
XX 06-JUL-2000.
XX
XX 24-DEC-1999; 99WO-N200228.
XX
XX 24-DEC-1998; 98NZ-0333589.
XX
XX (AUCC-) AUCCLAND UNISERVICES LTD.
XX
XX Fraser JD, Proft T;
XX
XX WPI; 2000-452370/39.
XX
XX N-PSDB; AAA47147.
XX
XX Novel superantigens from streptococcus pyogenes useful for genotyping
XX
XX streptococcus pyogenes clones expressing SMEZ-2 and for diagnosing a
XX
XX Kawasaki syndrome

XX PS Claim 2; Fig 2; 72pp; English.

CC The present sequence represents the SMEZ-2 superantigen protein. The

CC specification describes superantigen proteins SMEZ-2, SPE-G, SPE-H

CC and SPE-J. The superantigen polynucleotides and polypeptides are

CC used for subtyping Streptococci. They are also used for diagnosing

CC Streptococcal disease. The superantigens are used in diagnosis of

CC disease such as Kawasaki syndrome. They are also useful to recruit

CC and activate T cells in a relatively non-specific fashion since

CC they bind a large number of T cell receptor molecules by binding to the

CC Vbeta domain. Superantigen constructs are useful in cancer therapy.

XX Sequence 233 AA;

Query Match 100.0%; Score 1207; DB 21; Length 233;

Best Local Similarity 100.0%; Pred. No. 7.3e-101;

Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKTKLIFSFTSIFTAIISRVPFVGLVDNNSLLRNISTIVYVSDIVDFKTSNHLVTK 60

DB 1 MKKTKLIFSFTSIFTAIISRVPFVGLVDNNSLLRNISTIVYVSDIVDFKTSNHLVTK 60

QY 61 KLDVDRDARDFINSEMDEYAANDFKTGKIAVSVFPDWNLSKGVTAITYGGTTPYOK 120

DB 61 KLDVDRDARDFINSEMDEYAANDFKTGKIAVSVFPDWNLSKGVTAITYGGTTPYOK 120

QY 121 TSIPKNIPVNLWINGKQISVPYNEISTNKTVTTAQEIIDLKVRKFLIAHQHLYSSGSSYKS 180

DB 121 TSIPKNIPVNLWINGKQISVPYNEISTNKTVTTAQEIIDLKVRKFLIAHQHLYSSGSSYKS 180

QY 191 GRLVFHTNDNSDKYSFDFLYVGYRDKESIFKVKYKDNKSFNIDKIGHLDIEIDS 233

DB 191 GRLVFHTNDNSDKYSFDFLYVGYRDKESIFKVKYKDNKSFNIDKIGHLDIEIDS 233

RESULT 2

ABP29565

ID ABP29565 standard; Protein: 258 AA.

XX AC ABP29565;

XX DT 02-JUL-2002 (first entry)

XX DE Streptococcus polypeptide SEQ ID NO 8306.

XX KW Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;

XX KW group A streptococcus; Streptococcus pyogenes; antibacterial;

XX KW antinflammatory; infection; vaccine; meningitis; gene therapy.

XX OS Streptococcus pyogenes.

XX WO200234771-A2.

XX PD 02-MAY-2002.

XX PF 29-OCT-2001; 2001WO-GB04789.

XX PR 27-OCT-2000; 2000GB-0026333.

XX PR 24-NOV-2000; 2000GB-0028727.

XX PR 07-MAR-2001; 2001GB-0005640.

XX PA (CHIR-) CHIRON SPA.

XX PA (GENO-) INST GENOMIC RES.

XX PI Telford J, Masignani V, Margarit Ros YI, Grandi G, Fraser C;

XX PI Tetelin H;

XX DR WPI; 2002-352536/38.

XX DR N-PSDB; ABN70196.

XX PT New Streptococcus protein for the treatment or prevention of infection

XX OR disease caused by Streptococcus bacteria, such as meningitis, and

PT for detecting a compound that binds to the protein -

XX Claim 1; Page 3947; 4525pp; English.

XX The invention relates to a protein (ABP25413-ABP30895) from group B

CC Streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS

CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in

CC the specification. The proteins have antibacterial and antiinflammatory

CC activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and

CC antibodies that bind (I) are used in the manufacture of medicaments for

CC the treatment or prevention of infection or disease caused by

CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.

CC Nucleic acids encoding (I) are used to detect Streptococcus in a

CC biological sample. (I) is used to determine whether a compound binds to

CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be

CC used as a vaccine or diagnostic composition. The disease caused by

CC Streptococcus that is prevented or treated may be meningitis. Nucleic

CC acid encoding (I) may be used to recombinantly produce (I) and may be

CC used in gene therapy. Antibodies to (I) are used for affinity

CC chromatography, immunoassays, and distinguishing/identifying

CC Streptococcus proteins.

XX Sequence 258 AA;

Query Match 93.3%; Score 1126; DB 23; Length 258;

Best Local Similarity 92.7%; Pred. No. 1.7e-93;

Matches 216; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 1 MKKTKLIFSFTSIFTAIISRVPFVGLVDNNSLLRNISTIVYVSDIVDFKTSNHLVTK 60

DB 26 MKKTKLIFSFTSIFTAIISRVPFVGLVDNNSLLRNISTIVYVSDIVDFKTSNHLVTK 85

QY 61 KLDVDRDARDFINSEMDEYAANDFKTGKIAVSVFPDWNLSKGVTAITYGGTTPYOK 120

DB 86 KLDVDRDARDFINSEMDEYAANDFKTGKIAVSVFPDWNLSKGVTAITYGGTTPYOK 145

QY 121 TSIPKNIPVNLWINGKQISVPYNEISTNKTVTTAQEIIDLKVRKFLIAHQHLYSSGSSYKS 180

DB 146 EPMKSNIPVNLWINKQIPVPYINQISTNKTVTTAQEIIDLKVRKFLISQHLYSSGSSYKS 205

QY 181 GRLVFHTNDNSDKYSFDFLYVGYRDKESIFKVKYKDNKSFNIDKIGHLDIEIDS 233

DB 206 GRLVFHTNDNSDKYSFDFLYVGYRDKESIFKVKYKDNKSFNIDKIGHLDIEIDS 258

RESULT 3

ABP29257

ID ABP29257 standard; Protein: 235 AA.

XX AC ABP29257;

XX DT 02-JUL-2002 (first entry)

XX DE Streptococcus polypeptide SEQ ID NO 7690.

XX KW Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;

XX KW group A streptococcus; Streptococcus pyogenes; antibacterial;

XX KW antinflammatory; infection; vaccine; meningitis; gene therapy.

XX OS Streptococcus pyogenes.

XX WO200234771-A2.

XX PD 02-MAY-2002.

XX PF 29-OCT-2001; 2001WO-GB04789.

XX PR 27-OCT-2000; 2000GB-0026333.

XX PR 24-NOV-2000; 2000GB-0028727.

XX PR 07-MAR-2001; 2001GB-0005640.

XX PA (CHIR-) CHIRON SPA.

XX PA (GENO-) INST GENOMIC RES.

XX Telford J, Masignani V, Margarit Ros YI, Grandi G, Fraser C;
 PI Tettelein H;
 XX WPI: 2002-352536/38.
 DR N-PSDB; ABN69888.
 XX New Streptococcus protein for the treatment or prevention of infection
 PT or disease caused by Streptococcus bacteria, such as meningitis, and
 PT for detecting a compound that binds to the protein -
 XX Claim 1: Page 3906; 4525pp; English.
 XX The invention relates to a protein (ABP25413-ABP30895) from group B
 CC Streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS
 CC (Streptococcus pyogenes), comprising one of 5483 sequences (SI), given in
 CC the specification. The proteins have antibacterial and anti-inflammatory
 CC activity. (I), nucleic acids encoding (I), ABN6044-ABN71526 and
 CC antibodies that bind (I) are used in the manufacture of medicaments for
 CC the treatment or prevention of infection or disease caused by
 CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
 CC Nucleic acids encoding (I) are used to detect Streptococcus in a
 CC biological sample. (I) is used to determine whether a compound binds to
 CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be
 CC used as a vaccine or diagnostic composition. The disease caused by
 CC Streptococcus that is prevented or treated may be meningitis. Nucleic
 CC acid encoding (I) may be used to recombinantly produce (I) and may be
 CC used in gene therapy. Antibodies to (I) are used for affinity
 CC chromatography, immunoassays, and distinguishing/identifying
 CC Streptococcus proteins.
 XX Sequence 235 AA;
 SQ
 Query Match 25.3%; Score 305; DB 23; Length 235;
 Best Local Similarity 32.7%; Pred. No. 1.5e-19;
 Matches 80; Conservative 45; Mismatches 96; Indels 24; Gaps 9;
 QY 1 MKK---TKLIFSTSFIAISRPFVGLVDNNSLRNI-----YSTIVYEYSDIVID 50
 DB 1 MKKINIKIVITITVILISTIS-PI--IKSDSKDISNVKSDLLAYTITPYDKNCRVN 57
 QY 51 FKTSH--NLVTKKLDVRDARDFINSEMDYEAANDFKTGDKIAVFSVPDWNLSKGVY 108
 DB 58 FSTHTLNIDTKY---RGKDYIISSEMSYASQKFRDHDVDFGL----FYILNSHTG 110
 QY 109 AVTYGIGITPYQKTSIPKPNVNLWNGKOISVPYNEISTNKTVTQAQIDLVKVKFLIAQ 168
 DB 111 EYIGGITPAQNNKYNHKLGNLFISGESQOQNNKILKIDIVTFQEDFKIRKYLMDN 170
 QY 169 HOLYSSGSYKSGRLVFTHTNDSKYSFDLF-YVGYRDKESIFKVKYDNKSNFIDKIGHL 227
 DB 171 KYIDATSPYVSGRIEIGTKDGKHE-QIDLFDSNPNEGTRSDIFAKYKDNRIINMKNFSH 229
 QY 228 DIEID 232
 DB 230 DYILE 234
 RESULT 4
 ID AAW62787 standard; Protein; 235 AA.
 XX AAW62787;
 AC AAW62787;
 XX 24-SEP-1998 (first entry)
 DT Mutant streptococcal pyrogenic exotoxin type C (SPE-C).
 XX Streptococcus pyrogenic exotoxin type C; SPE-C toxin; STSS;
 KW streptococcal toxic shock syndrome; mutant; vaccine.
 XX Streptococcus pyrogenes.
 OS Streptococcus pyrogenes.
 XX

FH Key Location/Qualifiers
 FT Peptide 1..27
 FT Protein /note= "signal peptide"
 FT 28..235
 FT /note= "mature protein"
 FT optionally substituted with Ala"
 FT Misc-difference 42
 FT /label= Y15A
 FT /note= "Tyr at position 15 of the mature protein
 FT substituted with Ala"
 FT Misc-difference 65
 FT /label= N38A
 FT /note= "Asn at position 38 of the mature protein
 FT substituted with Ala"
 FT WO9824910-A2.
 XX 11-JUN-1998.
 XX 05-DEC-1997; 97WO-US22125.
 XX 06-DEC-1996; 96US-0033251.
 XX (MINU) UNIV MINNESOTA.
 XX Gahr PJ, Mitchell DT, Ohlendorf D, Schlievert PM;
 XX WPI: 1998-333329/29.
 PT Mutant non-lethal Streptococcus pyrogenic exotoxin type C - useful
 PT for vaccines to protect from biological activity of wild type toxin
 PT e.g. to prevent or ameliorate streptococcal toxic shock syndrome
 XX Claim 7; Page -: 55pp; English.
 CC The present sequence represents a mutant Streptococcus pyrogenic
 CC exotoxin type C (SPE-C) toxin. Streptococcus pyrogenes is a pathogen
 CC of humans which can cause mild infections e.g. impetigo or severe acute
 CC diseases SPE-C is thought to be associated with streptococcal toxic
 CC shock syndrome (STSS) and has several proposed biological activities,
 CC e.g. has been shown to block liver clearance of endotoxin and act
 CC as a "superantigen" i.e. induce T lymphocytes proliferation, resulting
 CC in abnormally high levels of circulating cytokines TNF- beta and
 CC IFN- gamma. The mutant toxins are useful in vaccines which can be
 CC administered to animals (especially humans) to protect against at
 CC least one biological activity of a wild-type SPE-C. Such vaccines are
 CC especially useful to reduce symptoms associated with toxic shock such
 CC as STSS in humans.
 CC note: this sequence does not appear in the specification; it was created
 CC using information provided.
 XX Sequence 235 AA;
 SQ
 Query Match 24.6%; Score 297; DB 19; Length 235;
 Best Local Similarity 31.7%; Pred. No. 8e-19;
 Matches 76; Conservative 40; Mismatches 110; Indels 14; Gaps 5;
 QY 1 MKTKLIFSTSFIAISRPFVGLVDNNSLRNI-----YSTIVYEYSDIVIDFKT 53
 DB 1 MKKINIKIVITITVILISTIS-PI--IKSDSKDISNVKSDLLAYTITPYDKNCRVN 60
 QY 54 SHNLVTKKLDVRDARDFINSEMDYEAANDFKTGDKIAVFSVPDWNLSKGVYATYTG 113
 DB 61 THTLAIDTKYR-GKDYIISSEMSYASQKFRDHDVDFGL----FYILNSHTGYIYG 115
 QY 114 GITPYQKTSIPKPNVNLWNGKOISVPYNEISTNKTVTQAQIDLVKVKFLIAQHLYS 173
 DB 116 GITPAQNNKYNHKLGNLFISGESQOQNNKILKIDIVTFQEDFKIRKYLMDNKIYD 175
 QY 174 SSSYKSGRLVFTHTNDSKYSFDLF-YVGYRDKESIFKVKYDNKSNFIDKIGHLIEID 232
 DB 176 ATSPYVSGRIEIGTKDGKHE-QIDLFDSNPNEGTRSDIFAKYKDNRIINMKNFSHFDIYLE 234

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RESULT 5
AAW62788
ID AAW62788 standard; Protein; 235 AA.
XX
XX
XX AAW62788;
XX
XX 24-SEP-1998 (first entry)
XX
XX Mutant streptococcal pyrogenic exotoxin type C (SPE-C).
DE Streptococcus pyrogenic exotoxin type C; SPE-C toxin; STSS;
KW Streptococcal toxic shock syndrome; mutant; vaccine.
XX
XX Streptococcus pyrogenes.
XX
XX Key Location/Qualifiers
FH Peptide 1..27
FT /note= "signal peptide"
FT Protein 28..235
FT /note= "mature protein"
FT /note= "optionally substituted with Ala"
FT Misc-difference 44
FT /label= Y17A
FT /note= "Tyr at position 17 of the mature protein
FT substituted with Ala"
FT Misc-difference 65
FT /label= N38A
FT /note= "Asn at position 38 of the mature protein
FT substituted with Ala"
XX
XX WO9824910-A2.
XX
XX 11-JUN-1998.
XX
XX 05-DEC-1997; 97WO-US22125.
XX
XX 06-DEC-1996; 96US-0033251.
XX
XX (MINU ) UNIV MINNESOTA.
XX
XX Gahr PJ, Mitchell DT, Ohlendorf D, Schlievert PM;
XX WPI; 1998-333329/29.
XX
XX Mutant non-lethal Streptococcus pyrogenic exotoxin type C - useful
XX for vaccines to protect from biological activity of wild type toxin
XX e.g. to prevent or ameliorate streptococcal toxic shock syndrome
XX
XX Claim 9; Page -: 55pp; English.
XX
XX The present sequence represents a mutant Streptococcus pyrogenic
XX exotoxin type C (SPE-C) toxin. Streptococcus pyrogenes is a pathogen
XX of humans which can cause mild infections e.g. impetigo or severe acute
XX diseases SPE-C is thought to be associated with streptococcal toxic
XX shock syndrome (STSS) and has several proposed biological activities,
XX e.g. has been shown to block liver clearance of endotoxin and act
XX as a "superantigen" i.e. induce T lymphocytes proliferation, resulting
XX in abnormally high levels of circulating cytokines TNF- beta and
XX IFN- gamma. The mutant toxins are useful in vaccines which can be
XX administered to animals (especially humans) to protect against at
XX least one biological activity of a wild-type SPE-C. Such vaccines are
XX especially useful to reduce symptoms associated with toxic shock such
XX as STSS in humans.
XX note: this sequence does not appear in the specification; it was created
XX using information provided.
XX
XX Sequence 235 AA:
XX
XX Query Match 24.6%; Score 297; DB 19; Length 235;
XX Best Local Similarity 31.7%; Pred. No. 8e-19;
XX Matches 76; Conservative 41; Mismatches 109; Indels 14; Gaps 5;

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QY 1 MKKTKLIFSETSIATISRPVGLVDNNSLLRNXYSTIV-----YVSVDIVDFKT 53
DB 1 MKKINIKIVITLITVILISTYFYHOSDSKKDISNKSDDLIAATITPYDKDCRVNFT 60
XX
XX 54 SHNLVTKKLDVRDARDFINSEMDYAAANDFKTGDKIAVFSVPDWNLYLSKGVYATYTG 113
DB 61 THTLAIDTQYR-GKDYVISSEMSYEASQFKRDRDHVDVFLG----FYILNSHTGEVIYG 115
XX
XX 114 GITPYQKTSIPKNIPVNLINGKQISVPYNEISTNKTTVTAAQETDLKVRFLIAHQHLYS 173
DB 116 GITPAQNNKVNHLKGLNLFISGESQQNLNKKIILEKIDIVTFOEIDFKIRKYLMDNYKIYD 175
XX
XX 174 SGSSYKSGRLVFHTNDNSDKYSFDLF-YVGYRDKESIFKVKDKNSFNIDKIGHLDIYD 232
DB 176 ATPYVSGRIEIGTKDGKHE-QIDLFDSPNEGTSDIFAKYKDNRIINMKNFHFDIYLE 234
XX
XX
XX RESULT 6
XX AAW62784
XX ID AAW62784 standard; Protein; 235 AA.
XX
XX AC AAW62784;
XX
XX 24-SEP-1998 (first entry)
XX
XX Streptococcal pyrogenic exotoxin type C (SPE-C).
XX
XX Streptococcus pyrogenic exotoxin type C; SPE-C toxin; STSS;
XX KW streptococcal toxic shock syndrome; mutant; vaccine.
XX
XX Streptococcus pyrogenes.
XX
XX Key Location/Qualifiers
FH Peptide 1..27
FT /note= "signal peptide"
FT Protein 28..235
FT /note= "mature protein"
XX
XX WO9824910-A2.
XX
XX 11-JUN-1998.
XX
XX 05-DEC-1997; 97WO-US22125.
XX
XX 06-DEC-1996; 96US-0033251.
XX
XX (MINU ) UNIV MINNESOTA.
XX
XX Gahr PJ, Mitchell DT, Ohlendorf D, Schlievert PM;
XX WPI; 1998-333329/29.
XX N-PSDB; AAW42209.
XX
XX Mutant non-lethal Streptococcus pyrogenic exotoxin type C - useful
XX for vaccines to protect from biological activity of wild type toxin
XX e.g. to prevent or ameliorate streptococcal toxic shock syndrome
XX
XX Disclosure; Fig 1; 55pp; English.
XX
XX The present sequence represents a Streptococcus pyrogenic exotoxin type
XX C (SPE-C) toxin. Streptococcus pyrogenes is a pathogen of humans which
XX can cause mild infections e.g. impetigo or severe acute diseases e.g.
XX scarlet fever and STSS. SPE-C is thought to be associated with
XX streptococcal toxic shock syndrome (STSS) and has several proposed
XX biological activities, e.g. has been shown to block liver clearance of
XX endotoxin and act as a "superantigen" i.e. induce T lymphocytes
XX proliferation, resulting in abnormally high levels of circulating
XX cytokines TNF- beta and IFN- gamma. The SPE-C protein is mutated (see
XX AAW62785-88) to make it substantially non-lethal compared to wild-type
XX SPE-C toxin. The mutant toxins are useful in vaccines which can be
XX administered to animals (especially humans) to protect against at least
XX one biological activity of a wild-type SPE-C. Such vaccines are
XX especially useful to reduce symptoms associated with toxic shock such as

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CC STSS in humans.
XX
SQ Sequence 235 AA;

Query Match 24.5%; Score 296; DB 19; Length 235;
Best Local Similarity 31.0%; Pred. No. 9.8e-19;
Matches 77; Conservative 42; Mismatches 105; Indels 10; Gaps

QY 1 MKKTKLIFSETSIATISRPVFCGLEVDNNSLLRNI-----YSTIVVEYSDIVIDEFT 53
   ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
DB 1 MKKNIKIIVITVILISTVFTYHQSDSKDISNVKSDLLIYATTPDYDKDCRVNFT 60

QY 54 SH--NLVTKKLDVARDARDFINSEMEDEYAANDFKTGKIAVSPFEDWNYLSKGKVTAYT 111
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
DB 61 THTLNDITQRY--RGKDYIISSEMSYEASQKFKRDDHVDVFL-----FVILNHSHTGEVI 113

QY 112 YGGITPQKTSIPKNIPVNLWINGKOISVPYNEISTNKTVTQAETDLVKRFELIAHQHL 171
   ||||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
DB 114 YGGITPAQNNKVNHKLLGNLFISGESQONLNKILIEKDIVTFOEIDFKIRKYLMDNYKI 173

QY 172 YSGSSYKSGRLVHFHNDNSDKYSFDLF-YVGYRDKESIFKVKYDKNKSFNIDKIGHLDI 230
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
DB 174 YDATSPVYSGRIEIGYKDGKHE-QIDLFSPNEGTRSDIFAKYKDNRIINMKNFSEFDIY 232

QY 231 ID 232
DB 233 LE 234

RESULT 7
AAR13210
ID AAR13210 standard; Protein; 208 AA.
XX
AC AAR13210;
XX
DT 15-OCT-1991 (first entry)
XX
DE Streptococcal pyrogenic enterotoxin C.
XX
KW SPE C; cancer treatment; pyrogen; tumouricide; scarlet fever.
XX
OS Streptococcus NY-5 strain.
XX
PN WO9110680-A.
XX
PD 25-JUL-1991.
XX
PF 17-JAN-1991; 91WO-US00342.
XX
PR 17-JAN-1990; 90US-0466577.
XX
(TERM/) TERMAN D S.
XX
Terman DS;
XX
WPI; 1991-237984/32.
XX
Treating cancer with enterotoxin from Staphylococcus aureus -
administered by IV injection, having same tumoricidal activity
as Staphylococcal protein A without potential toxic reactions
XX
PS Disclosure; Fig 1; 74pp; English.
XX
SPE C can be used for tumoricidal treatment, esp. with a haemolysin.
CC Synthetic polypeptides having structural homology to Streptococcal
CC pyrogenic exotoxins are claimed, provided the homology includes
CC statistically significant sequence homology, alignment of Cysteine
CC residues and similar hydropathy profiles.
CC See AAR13203-R13211.
XX
SQ Sequence 208 AA;

Query Match 23.7%; Score 285.5; DB 12; Length 208;

```


CC tumoricidal reaction.
 XX
 SQ Sequence 208 AA; 23.7%; Score 285.5; DB 23; Length 208;
 Query Match 34.2%; Pred. No. 7.4e-18;
 Best Local Similarity 35; Mismatches 85; Indels 11; Gaps 5;
 Matches 68; Conservative 35; Mismatches 85; Indels 11; Gaps 5;

QY 37 YSTIVVEYSDIVDFKTS--NLVTKLDVDRDFFINSEMDYAAANDFKTGKIAVFS 94
 Db 17 YTPDYDKRVNFTWLNIDTQY---RGKDYISSEMSYEAQKFRDDHVDVFG 73
 QY 95 VPEDWNLKSGKVATYGGITPYQKTSIPKNIPIVNLWINGKOISVPYNEISTNKTVTVA 154
 Db 74 L----FYILNSHRTGEYTGITPAQNNKVNHLGNLFISGESQOENLNKILKIDVTF 129
 QY 155 QEIDLKVRKELIAHQHLYSSGSKSLRVFHTNDNDKYSFDLF-VGYRDRKESIFKY 213
 Db 130 QEIDFKIRKYLMDNYKIYDTSYVSGRIEIGTKDGKHE-QIDLFDSPNEGTRSDIFAKY 188
 QY 214 KKNKSNIDKIGHLDIHD 232
 Db 189 KDNRIINMKNFHFIDYLE 207

RESULT 11
 AAW62785
 ID AAW62785 standard; Protein; 235 AA.
 AC AAW62785;
 XX
 DT 24-SEP-1998 (first entry)
 DE Mutant streptococcal pyrogenic exotoxin type C (SPE-C).
 XX
 KW Streptococcus pyrogenic exotoxin type C; SPE-C toxin; STSS;
 KW streptococcal toxic shock syndrome; mutant; vaccine.
 XX
 OS Streptococcus pyrogenes.
 XX

Key Location/Qualifiers
 FT Peptide 1..27
 FT /note= "signal peptide"
 FT Protein 28..235
 FT /note= "mature protein"
 FT Misc-difference 39
 FT /note= "Asp at position 12 of the mature protein
 FT optionally substituted with Ala, Glu, Asn,
 FT Gln, Lys, Arg, Ser or Thr"
 FT Misc-difference 42
 FT /note= "Tyr at position 15 of the mature protein
 FT optionally substituted with Phe, Ala, Gly,
 FT Ser or Thr"
 FT Misc-difference 44
 FT /note= "Tyr at position 17 of the mature protein
 FT optionally substituted with Phe, Ala, Gly, Glu,
 FT Lys, Arg, Asp, Ser or Thr"
 FT Misc-difference 62
 FT /note= "His at position 35 of the mature protein
 FT optionally substituted with Phe, Ala, Gly, Glu,
 FT Lys, Arg, Asp, Ser, Tyr or Thr"
 FT Misc-difference 65
 FT /note= "Asn at position 38 of the mature protein
 FT optionally substituted with Ala, Asp, Glu,
 FT Lys or Arg"
 FT Misc-difference 162
 FT /note= "Lys at position 135 of the mature protein
 FT optionally substituted with Asp or Glu"
 FT Misc-difference 165
 FT /note= "Lys at position 138 of the mature protein
 FT optionally substituted with Asp or Glu"
 FT Misc-difference 166
 FT /note= "Tyr at position 139 of the mature protein

optionally substituted with Phe, Ala, Gly,
 Glu, Lys, Arg, Asp, Ser or Thr"
 /note= "Asp at position 142 of the mature protein
 optionally substituted with Ala, Glu,
 Gln, Lys, Arg, Asn, Ser or Thr"
 WO9824910-A2.
 11-JUN-1998.
 05-DEC-1997; 97WO-US22125.
 06-DEC-1996; 96US-0033251.
 (MINU) UNIV MINNESOTA.
 Gahr PJ, Mitchell DT, Ohlendorf D, Schlievert PM;
 WPI; 1998-333329/29.
 Mutant non-lethal Streptococcus pyrogenic exotoxin type C - useful
 for vaccines to protect from biological activity of wild type toxin
 e.g. to prevent or ameliorate streptococcal toxic shock syndrome
 Claim 4; Page 1; 55pp; English.
 The present sequence represents a mutant Streptococcus pyrogenic
 exotoxin type C (SPE-C) toxin. Streptococcus pyrogenes is a pathogen
 of humans which can cause mild infections e.g. impetigo or severe acute
 diseases SPE-C is thought to be associated with streptococcal toxic
 shock syndrome (STSS) and has several proposed biological activities,
 e.g. has been shown to block liver clearance of endotoxin and act
 as a "superantigen" i.e. induce T lymphocytes proliferation, resulting
 in abnormally high levels of circulating cytokines TNF- beta and
 IFN- gamma. The mutant toxins are useful in vaccines which can be
 administered to animals (especially humans) to protect against at
 least one biological activity of a wild-type SPE-C. Such vaccines are
 especially useful to reduce symptoms associated with toxic shock such
 as STSS in humans.
 CC note: this sequence does not appear in the specification; it was created
 using information provided.

Query Match 22.7%; Score 274; DB 19; Length 235;
 Best Local Similarity 30.4%; Pred. No. 9.5e-17;
 Matches 73; Conservative 40; Mismatches 113; Indels 14; Gaps 5;
 QY 1 MKTKLIFSFTSIFIAISRPVFGLEVNDNNLSLRNIVSTIV-----YEYSDIVIDPKT 53
 Db 1 MKKNIHIVFIITVILISTYFTYHQSDKKDISNKSXLLXATITPYDYKOCRVNFT 60
 QY 54 SHNLVTKLDVDRDFFINSEMDYAAANDFKTGKIAVFSVPEDWNLKSGKVATYTG 113
 Db 61 TTXLXIDTQKVR-KEDYISSEMSYEAQKFRDDHVDVFGL-----FYILNSHRTGEYTG 115
 QY 114 GITPYQKTSIPKNIPIVNLWINGKOISVPYNEISTNKTVTVAQEIIDLKVRKELIAHQHLYS 173
 Db 116 GITPAQNNKVNHLGNLFISGESQOENLNKILKIDVTFQEIIDFIRXKLKMYKIYD 175
 QY 174 SGSSYKSGRLVPHFHTNDNDKYSFDLF-VGYRDRKESIFKYKDNKSNIDKIGHLDIHD 232
 Db 176 ATPSYVSGRIEIGTKDGKHE-QIDLFDSPNEGTRSDIFAKYKDNRIINMKNFHFIDYLE 234

RESULT 12
 AAW62786
 ID AAW62786 standard; Protein; 235 AA.
 XX
 AC AAW62786;
 XX
 DT 24-SEP-1998 (first entry)

XX DE Mutant streptococcal pyrogenic exotoxin type C (SPE-C).
 XX KW Streptococcus pyrogenic exotoxin type C; SPE-C toxin; STSS;
 XX KW streptococcal toxic shock syndrome; mutant; vaccine.
 XX OS Streptococcus pyrogenes.
 PH Key Location/Qualifiers
 FT Peptide 1..27
 FT Protein 28..235
 FT Misc-difference 39 /note= "mature protein"
 FT /label= D12A
 FT /note= "Asp at position 12 of the mature protein
 FT optionally substituted with Ala"
 FT Misc-difference 42 /label= Y15A
 FT /note= "Tyr at position 15 of the mature protein
 FT optionally substituted with Ala"
 FT Misc-difference 44 /label= Y17A
 FT /note= "Tyr at position 17 of the mature protein
 FT optionally substituted with Ala"
 FT Misc-difference 62 /label= H35A
 FT /note= "His at position 35 of the mature protein
 FT optionally substituted with Ala"
 FT Misc-difference 65 /label= N38D
 FT /note= "Asn at position 38 of the mature protein
 FT optionally substituted with Asp"
 FT Misc-difference 162 /label= K135D
 FT /note= "Lys at position 135 of the mature protein
 FT optionally substituted with Asp"
 FT Misc-difference 165 /label= K138D
 FT /note= "Lys at position 138 of the mature protein
 FT optionally substituted with Asp"
 FT Misc-difference 166 /label= Y139A
 FT /note= "Tyr at position 139 of the mature protein
 FT optionally substituted with Ala"
 FT Misc-difference 169 /label= D142N
 FT /note= "Asp at position 142 of the mature protein
 FT optionally substituted with Asn"
 XX WO9824910-A2.
 XX 11-JUN-1998.
 XX 05-DEC-1997; 97WO-US22125.
 XX 06-DEC-1996; 96US-0033251.
 XX (MINU) UNIV MINNESOTA.
 XX Gahr PJ, Mitchell DT, Ohlendorf D, Schlievert PM;
 XX WPI; 1998-333329/29.
 XX Mutant non-lethal Streptococcus pyrogenic exotoxin type C - useful
 XX for vaccines to protect from biological activity of wild type toxin
 XX e.g. to prevent or ameliorate streptococcal toxic shock syndrome
 XX Claim 5; Page -: 55pp; English.
 XX The present sequence represents a mutant Streptococcus pyrogenic
 XX exotoxin type C (SPE-C) toxin. Streptococcus pyrogenes is a pathogen
 XX of humans which can cause mild infections e.g. impetigo or severe acute

CC diseases SPE-C is thought to be associated with streptococcal toxic
 CC shock syndrome (STSS) and has several proposed biological activities,
 CC e.g. has been shown to block liver clearance of endotoxin and act
 CC as a "superantigen" i.e. induce T lymphocytes proliferation, resulting
 CC in abnormally high levels of circulating cytokines TNF- beta and
 CC IFN- gamma. The mutant toxins are useful in vaccines which can be
 CC administered to animals (especially humans) to protect against at
 CC least one biological activity of a wild-type SPE-C. Such vaccines are
 CC especially useful to reduce symptoms associated with toxic shock such
 CC as STSS in humans.
 CC note: this sequence does not appear in the specification; it was created
 CC using information provided.

XX Sequence 235 AA;

Query Match 22.4%; Score 270; DB 19; Length 235;
 Best Local Similarity 30.6%; Pred. No. 2.2e-16;
 Matches 74; Conservative 41; Mismatches 109; Indels 18; Gaps 6;

QY 1 MKKTKLIFSFTSIFTAISRVPVGLVNNLSLLRNIYSTIV-----YEYSDIVIDFKT 53
 DB 1 MKKINIKIVFIITVILISTYTYTHQSDSKDISNVKALLAAATTPDYDKCRVNFST 60
 QY 54 SHNLVTKLDVRDAR--DFFINSEMDVAANDFKGTAVSFVDFDWNLYSKGKVTAT 111
 DB 61 T---ATLDDIDYQKRGKDYIISSEMSYASQFKKRDHVDVFL----FIILNSTGETI 113
 QY 112 YGGITPYQKTSIPKNIPVNLWMINGKQISVPYNEISNTKTITVTAQIDILKVRFLIAQHOL 171
 DB 114 YGGITPAQNKNVNHKLLGNLFTSGSQQLNNKIILEKDIVTFQIEDFDIRDALNNYKI 173
 QY 172 YSSGSYKSGRLVFTNDSKYSFDLF-YVGYRDKESIFKYVKNKSNFNDIKIGHLDIE 230
 DB 174 YDATSPYVSGRIEIGTKDGKHE-QIDLFDSNEGTRSDIFAKYKDNRIINMKNFSHFDIY 232
 QY 231 ID 232
 DB 233 LE 234

RESULT 13

ABP29143
 ID ABP29143 standard; Protein; 232 AA.

AC ABP29143;

XX 02-JUL-2002 (first entry)

DE Streptococcus polypeptide SEQ ID NO 7462.

XX Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;
 KW group A streptococcus; Streptococcus pyogenes; antibacterial;
 KW antiinflammatory; infection; vaccine; meningitis; gene therapy.

OS Streptococcus pyogenes.

XX WO200234771-A2.

XX 02-MAY-2002.

XX 29-OCT-2001; 2001WO-GB04789.

XX 27-OCT-2000; 2000GB-0026333.

PR 24-NOV-2000; 2000GB-0028727.

PR 07-MAR-2001; 2001GB-0005640.

XX (CHIR-) CHIRON SPA.

PA (GENO-) INST GENOMIC RES.

XX Telford J, Masignani V, Margarit Ros YI, Grandi G, Fraser C;

PI Tettelin H;

XX WPI; 2002-352536/38.

DR N-PSDB; ABN69774.

XX New Streptococcus protein for the treatment or prevention of infection

PT or disease caused by Streptococcus bacteria, such as meningitis, and

PT for detecting a compound that binds to the protein -

XX

PS Claim 1; Page 3891; 4525pp; English.

XX

CC The invention relates to a protein (ABP25413-ABP30895) from group B

CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS

CC (Streptococcus pyogenes), comprising one of 5483 sequences (SI), given in

CC the specification. The proteins have antibacterial and antiinflammatory

CC activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and

CC antibodies that bind (I) are used in the manufacture of medicaments for

CC the treatment or prevention of infection or disease caused by

CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.

CC Nucleic acids encoding (I) are used to detect Streptococcus in a

CC biological sample. (I) is used to determine whether a compound binds to

CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be

CC used as a vaccine or diagnostic composition. The disease caused by

CC Streptococcus that is prevented or treated may be meningitis. Nucleic

CC acid encoding (I) may be used to recombinantly produce (I) and may be

CC used in gene therapy. Antibodies to (I) are used for affinity

CC chromatography, immunoassays, and distinguishing/identifying

CC Streptococcus proteins.

XX

SQ Sequence . 232 AA;

Query Match 21.5%; Score 259; DB 23; Length 232;

Best Local Similarity 29.7%; Pred. No. 2.1e-15;

Matches 68; Conservative 41; Mismatches 102; Indels 18; Gaps 7;

QY 11 TSFTAIISRPVFGLEVDNNSL-----LRNIYSTIVYEYSDIVDFKTSNHLVTKKLDV 64

DB 7 TILVLIIFHGVSASDSENKDKVQLNAYEIIIPVDITNCNIDYLTTHDFY---IDI 63

QY 65 RD--ARDFTINSEMDYAAADFDTGDKIAVFSVPFDWNLVSKGKVTAYTYGGITP-YQKT 121

DB 64 SSVKKNFSDSEVESYITTKFKNGKVNIFGLP----YIFTRYDVYIYGGVTPSVNSN 119

QY 122 STPKNIPVNLWNGKQISVPYNEISTNKTVTVAQEDLKVRFELIAHQHLYSSGSSYKSG 181

DB 120 SENSIVGNLLIDGVQOKTLINPKIDKPIFTIQEFDKIRQVLMQTYKIYDNPSPYIKG 179

QY 182 RVEHFNDSKYSPLF-YVGVRKESIFKYVKONKSNIDKIGHLDI 229

DB 180 QLEIAINGKHE-SFNLIDATSSSTRSDIFKFKYKDKNTINMKDFSHFDI 227

RESULT 14

AAU14103

ID AAU14103 standard; peptide; 257 AA.

XX

AC AAU14103;

XX

DT 21-NOV-2001 (first entry)

XX

DE Peptide sequence from Staphylococcus aureus enterotoxin type E.

XX

KW Anti-retroviral; DP178-like; DP107-like; enterotoxin type E;

XX

KW antifusogenic; antiviral; HIV transmission.

XX

OS Staphylococcus aureus.

XX

PN WO200151673-A2.

XX

PD 19-JUL-2001.

XX

PF 05-JUL-2000; 2000WO-US35727.

XX

PR 09-JUL-1999; 99US-0350841.

XX

PA (TRIM-) TRIMERIS INC.

XX

PI Jeffs P, Lackey JW, Erickson JB, Lawless MK, Merutka G;

XX

DR WPI; 2001-442157/47.

XX

PT Identifying a compound that inhibits the formation of or disrupts a

PT DP107/DP178 complex, especially compounds with antifusogenic, antiviral

PT or intracellular modulatory activity, by detecting the formation of a

PT DP107/DP178 complex -

XX

PS Disclosure; Fig 41; 259pp; English.

XX

CC The present invention relates to peptides which exhibit anti-retroviral

CC activity. The peptides of the invention (AAU12559-AAU14009) comprise

CC DP178-like and DP107-like peptides. The DP178 peptide corresponds

CC to amino acids 639-673 of the transmembrane protein gp1 from human

CC immunodeficiency virus 1 (HIV-1) isolate LAI. The DP107 peptide

CC corresponds to amino acids 558-595 of gp41 from HIV-1LAI. The invention

CC also relates to a method of identifying compounds that inhibit the

CC formation of or disrupts a DP107/DP178 complex. The method comprises

CC detecting the formation of a DP107/DP178 complex, both in the presence

CC or absence of a test compound, in a reaction mixture containing DP107

CC and DP178 peptides. The method is useful for identifying compounds,

CC including small molecule compounds, which may themselves exhibit

CC antifusogenic, antiviral or intracellular modulatory activity. The

CC DP178-like/DP107-like peptides are useful to inhibit human and non-human

CC retroviral, particularly HIV, transmission to uninfected cells. The

CC present sequence represents a peptide sequence from Staphylococcus aureus

CC enterotoxin type E.

XX

SQ Sequence 257 AA;

Query Match 21.4%; Score 258.5; DB 22; Length 257;

Best Local Similarity 26.4%; Pred. No. 2.7e-15;

Matches 75; Conservative 55; Mismatches 67; Indels 87; Gaps 13;

QY 1 MKTKLIFSFTSIFIA--IISRPVFG-----LEVDNNSL--LRNIY--- 37

DB 1 MKTAFIL---LFIALTITTSPLVNGSESEINEKDLRKKSELOALNSLNLRQIYYN 57

QY 38 -----STIYVE-----YSDIVDFKTSNHLVTKKLDVDRDARDFIN 73

DB 58 EKAITENKESDDQFLENTLLFKGFTGHPWYNLLVD-----LGSKDATNKYKG 106

QY 74 SEMDEVAANDFKTGDKIAVFSVPFDWNLVSKG---KVTATYGGITPYQKTSI--PKNIP 128

DB 107 KVDLYGAY-----YGYOCAGGTPNKTACMYGGVTLHDNNRUTEKKVP 150

QY 129 VNLWNGKQISVPYNEISTNKTVTVAQEDLKVRFELIAHQHLYSS---GSSYKSGRLVF 185

DB 151 INLWIDGKQTTVPIDKVKTSKKEVTQVELDQARHYLHGKFGLYNSDSFGKVGQRLIVF 210

QY 186 HTNDSKYSFDFLYVGYRDKESIFKYVKONKSNIDKIGHLDI 229

DB 211 HSSEGS-TVSYDLFDAQGQYPTLLRIYRDNKTINSNL-HIDL 252

RESULT 15

AAU67339

ID AAB67339 standard; peptide; 230 AA.

XX

AC AAB67339;

XX

DT 23-APR-2001 (first entry)

XX

DE Staphylococcus aureus enterotoxin E protein.

XX

KW Tumour; cancer; immune; enterotoxin.

XX

OS Staphylococcus aureus.

XX

PN US6180097-B1.

XX

